

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 12, 2004, 11:11:35 ; Search time 21 Seconds
(without alignments)
3041.484 Million cell updates/sec

Title: US-10-087-217A-8
Perfect score: 3475
Sequence: 1 MMTKXNGVKSSPANNHH.....NHEDDVLSDGINTPTAAE 664

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3449	99.3	664	2 S11517	cyclic nucleotide-
2	3231.5	93.0	732	2 S35891	cyclic nucleotide-
3	3204.5	92.2	663	2 S11521	cAMP-gated channel
4	2219.5	63.9	735	2 I50630	alpha subunit of c
5	2140	61.6	706	2 A55251	cyclic nucleotide-
6	2131	61.3	682	1 JH0560	cyclic nucleotide-
7	2126.5	61.2	695	2 S74179	cyclic nucleotide-
8	2067	59.5	645	2 I50680	alpha subunit of r
9	2044	58.6	690	1 S07103	cAMP-gated ion cha
10	2035	58.6	686	1 A44842	cAMP-gated ion cha
11	2030	58.4	630	2 A42161	cAMP-gated cation
12	2017.5	58.1	691	2 JC6509	rod cyclic nucleot
13	1995.5	57.4	688	2 B42161	cAMP-gated cation
14	1518	43.7	575	2 I59327	olfactory cyclic n
15	1487	42.8	665	2 S52072	DmCNGC protein - f
16	1337	38.5	772	2 S28292	hypothetical prote
17	1323	38.1	261	2 I78559	cyclic nucleotide-
18	1160	33.4	261	2 I78560	cyclic nucleotide-
19	866.5	24.9	673	2 T20936	hypothetical prote
20	835	24.0	800	2 T19627	hypothetical prote
21	831	23.9	644	2 T33125	hypothetical prote
22	778	22.4	909	2 S32538	cAMP-gated cation
23	767.5	22.1	611	2 T20935	hypothetical prote
24	596.5	17.2	191	2 S74158	cAMP-gated cation
25	595.5	17.1	189	2 S74159	cAMP-gated cation
26	557.5	16.0	767	2 T21969	hypothetical prote
27	424.5	12.2	962	2 I53197	potassium channel
28	417	12.0	989	2 I48912	potassium channel
29	413	11.9	1102	2 T17367	potassium channel

30	407.5	11.7	1284	2 T13168	probable potassium
31	404.5	11.6	1174	2 A40853	potassium channel
32	395	11.4	1087	2 T31100	probable potassium
33	394	11.3	1159	2 I38465	hypothetical prote
34	382.5	11.0	514	2 T19579	probable potassium
35	380.5	10.9	1017	2 T31354	potassium channel
36	377.5	10.9	688	2 S55349	cyclic nucleotide-
37	376	10.8	716	2 T51354	potassium channel
38	359.5	10.3	662	2 T04461	potassium channel
39	353.5	10.2	934	2 T42394	probable potassium
40	350.5	10.1	845	2 T07052	potassium channel
41	347	10.0	828	2 T52046	probable calmoduli
42	345	9.9	702	2 T04424	hypothetical prote
43	341	9.8	738	2 E86294	cyclic nucleotide
44	337	9.7	698	2 T10541	potassium channel
45	336	9.7	787	2 S68699	potassium channel

ALIGNMENTS

RESULT 1

S11517
cyclic nucleotide-activated channel protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 13-Aug-1999
C:Accession: S11517
R:Dhalan, R.S.; Yau, K.W.; Schrader, K.A.; Reed, R.R.
Nature 347, 184-187, 1990
A:Title: Primary structure and functional expression of a cyclic nucleotide-activated (C)Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide; C:Keywords: Transmembrane protein
F:456-580/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP:
A:Accession: S11517
A:Molecule type: mRNA
A:Residues: 1-664 <DHA>
A:Cross-references: GB:X55519; NID:G56791; PID:CAA39135.1; PID:G56792
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide; C:Keywords: Transmembrane protein
F:456-580/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP:

Query Match 99.3%; Score 3449; DB 2; Length 664;
Best Local Similarity 99.5%; Pred. No. 7.1e-235;
Matches 661; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	MMTEKXNGVKSSPANNHHPPPSIKANGKDDHRAGSRPOSVAADDDTSPQLQRLAEMDT	60
Db	1	MMTEKXNGVKSSPANNHHPPPSIKANGKDDHRAGSRPOSVAADDDTSPQLQRLAEMDT	60
Qy	61	PRGRGGGFORIVRLGVIRDWANKNPREBEPDPSFLERPRGPELQTVTTHQGDGKGKD	120
Db	61	PRGRGGGFORIVRLGVIRDWANKNPREBEPDPSFLERPRGPELQTVTTHQGDGKGKD	120
Qy	121	GEKGTKKKFELFVLDPAQDWYRMLFVIAMPVLYNKCILLVARACSDIQRNFFVWLVVL	180
Db	121	GEKGTKKKFELFVLDPAQDWYRMLFVIAMPVLYNKCILLVARACSDIQRNFFVWLVVL	180
Qy	181	DYFSDTVYADLIIRLTGTFLEQGLLVKOPKRLRDNYIHTQFKLDVASIIPFDLIYFV	240
Db	181	DYFSDTVYADLIIRLTGTFLEQGLLVKOPKRLRDNYIHTQFKLDVASIIPFDLIYFV	240
Qy	241	GIHSPVFRNRLAHFARMPEFFDRTETRTSYNPIFRISNLVLYLVIHWNACIYYVISK	300
Db	241	GIHSPVFRNRLAHFARMPEFFDRTETRTSYNPIFRISNLVLYLVIHWNACIYYVISK	300
Qy	301	SIGFGVDTWYPIITDPEGYLAREYICLYNWTSLTITIGETPPPVKDEYLVFVDFEL	360
Db	301	SIGFGVDTWYPIITDPEGYLAREYICLYNWTSLTITIGETPPPVKDEYLVFVDFEL	360
Qy	361	IGVLIIFATIVGVNMGSMISNNATRAEFQAKIDAVKHYMOPRKYSKQWEAKVIKWFYLT	420
Db	361	IGVLIIFATIVGVNMGSMISNNATRAEFQAKIDAVKHYMOPRKYSKQWEAKVIKWFYLT	420
Qy	421	NKKTVDEREVLKKNLPAKLRABIAINVHLSTLTKKVRIFQDWEAGLVVLKLRPQVSPG	480
Db	421	NKKTVDEREVLKKNLPAKLRABIAINVHLSTLTKKVRIFQDWEAGLVVLKLRPQVSPG	480

Db 421 NKKTVDEREVLKMLPAKRAEIAINVHLSLTKKVRIFQDCEAGLLVELVLKLRPQVSPG 480
 QY 481 DYICRGDYGKEMYYIKGKLAIVADDGVTQYALLSAGSCFGEISILINIKSGKMGNRRTAN 540
 Db 481 DYICRGDYGKEMYYIKGKLAIVADDGVTQYALLSAGSCFGEISILINIKSGKMGNRRTAN 540
 QY 541 NIRSGLYSDFCLSKDLMKMEAVTEAPDAKKVLEERGREILMKMGLLDENEVAASMEVDVQ 600
 Db 541 NIRSGLYSDFCLSKDLMKMEAVTEAPDAKKVLEERGREILMKMGLLDENEVAASMEVDVQ 600
 QY 601 EKLEQLETNMDTLYTRFARLLAETGAQKQKORITVLETKMKQNHEDDYLSDGINTPEP 660
 Db 601 EKLEQLETNMDTLYTRFARLLAETGAQKQKORITVLETKMKQNHEDDYLSDGINTPEP 660
 QY 661 TAAE 664
 Db 661 TAAE 664
 RESULT 2
 S35691
 Cyclic nucleotide-gated channel protein - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
 C:Accession: S35691
 R:Biel, M.; Altenhofen, W.; Hüllin, R.; Ludwig, J.; Freichel, M.; Flockerzi, V.; Dascal, R.;
 FEBS Lett. 329, 134-138, 1993
 A:Title: Primary structure and functional expression of a cyclic nucleotide-gated channel
 A:Reference number: S35691; MUID:93359035; PMID:7689061
 A:Accession: S35691
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-732 <BI>
 A:Cross-references: EMBL:X59668; NID:9433959; PIDN:CAA42201.1; PID:9433960
 C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
 P:522-646/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>
 Query Match 93.0%; Score 3231.5; DB 2; Length 732;
 Best Local Similarity 93.8%; Pred. No. 1.7e-219;
 Matches 622; Conservative 16; Mismatches 24; Indels 1; Gaps 1;
 QY 2 MTEKNGVKSSPANNHHPPPSIKANGKDDHRRAGSRPOSVAADDTSPQLQRLAEMDTP 61
 Db 69 MTEKNGVKSSPANNHHPPATIKANGKDESTRSPOS-AADDTSELQRLAEMDAP 127
 QY 62 RRGRGGFORIVRLGVIRDWANKNFRPEPRPDSFLERFRGPELQVTTHQGDGKGDG 121
 Db 128 QQRGGFRIVRLGVIRQWANKNFRPEPRPDSFLERFRGPELQVTTHQGDGKGDG 187
 QY 122 EKGTKKKFELFVLDPAQDWYRWLFVIAAMPVLYNWCLLVARACFSDLQRYFVWLVLD 181
 Db 188 DKGTKKKFELFVLDPAQDWYRWLFVIAAMPVLYNWCLLVARACFSDLQRYFVWLVLD 247
 QY 182 YFSDTVYIADLIIRLTGTGLEQLAVKPKLRDNYIHTLOPKLDVASIIPDLYFAVG 241
 Db 248 YFSDVVIADLFIRLTGTGLEQLAVKPKLRDNYIHTLOPKLDVASIIPDLYFAVG 307
 QY 242 IHSPEVRFNRLHFARMFEFFDRTETRTSYPNIFRISNLVLYLVIHWNACIYYVVISKS 301
 Db 308 IHNPEVRFNRLHFARMFEFFDRTETRTSYPNIFRISNLVLYLVIHWNACIYYAISK 367
 QY 302 IGFGVDTWYVNIPTDEYGLAREYIYCLYWSLTLLTTIGETPPPVKDEYLFVIFDFLI 361
 Db 368 IGFGVDTWYVNIPTDEYGLAREYIYCLYWSLTLLTTIGETPPPVKDEYLFVIFDFLI 427
 QY 362 GVLIIFATIVGNVSMISNNMATAEFAQKIDAVKHYMQFRKVKSKMEAKVWKDFYLTWN 421
 Db 428 GVLIIFATIVGNVSMISNNMATAEFAQKIDAVKHYMQFRKVKSKMEAKVWKDFYLTWN 487
 QY 422 KKTVDREVLKMLPAKRAEIAINVHLSLTKKVRIFQDWEAGLLVELVLKLRPQVSPGD 481
 Db 488 KKTVDREVLKMLPAKRAEIAINVHLSLTKKVRIFQDCEAGLLVELVLKLRPQVSPGD 547

QY 482 YICRGDYGKEMYYIKGKLAIVADDGVTQYALLSAGSCFGEISILINIKSGKMGNRRTAN 541
 Db 548 YICRGDYGKEMYYIKGKLAIVADDGVTQYALLSAGSCFGEISILINIKSGKMGNRRTAN 607
 QY 542 IIRSLGYSDFCLSKDLMKMEAVTEAPDAKKVLEERGREILMKMGLLDENEVAASMEVDVQ 601
 Db 608 IIRSLGYSDFCLSKDLMKMEAVTEAPDAKKVLEERGREILMKMGLLDENEVAASMEVDVQ 667
 QY 602 KLEQLETNMDTLYTRFARLLAETGAQKQKORITVLETKMKQNHEDDYLSDGINTPEP 661
 Db 668 KLEQLETNMDTLYTRFARLLAETGAQKQKORITVLETKMKQNHEDDYLSDGINTPEP 727
 QY 662 TAAE 664
 Db 728 TAAE 730
 RESULT 3
 S11521
 CAMP-gated channel protein - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
 C:Accession: S11521
 R:Ludwig, J.; Margalit, T.; Bismann, E.; Lancet, D.; Kaupp, U.B.
 FEBS Lett. 270, 24-29, 1990
 A:Title: Primary structure of cAMP-gated channel from bovine olfactory epithelium.
 A:Reference number: S11521; MUID:91032022; PMID:1699793
 A:Accession: S11521
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-663 <LU>
 A:Cross-references: GB:X55010; NID:9287743; PIDN:CAA38754.1; PID:9287744
 C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide
 P:454-578/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>
 Query Match 92.2%; Score 3204.5; DB 2; Length 663;
 Best Local Similarity 92.3%; Pred. No. 1.2e-217;
 Matches 610; Conservative 27; Mismatches 23; Indels 1; Gaps 1;
 QY 2 MTEKNGVKSSPANNHHPPPSIKANGKDDHRRAGSRPOSVAADDTSPQLQRLAEMDTP 61
 Db 1 MTEKANGVKSSPANNHHPPAIKASGKDDHRRASRPQSAIAA-DTSSSELQRLAEMDAP 59
 QY 62 RRGRGGFORIVRLGVIRDWANKNFRPEPRPDSFLERFRGPELQVTTHQGDGKGDG 121
 Db 60 QQRGGFRIVRLGVIRLWAYRNFRPEPRPDSFLERFRGPELQVTTHQGDGKGDG 119
 QY 122 EKGTKKKFELFVLDPAQDWYRWLFVIAAMPVLYNWCLLVARACFSDLQRYFVWLVLD 181
 Db 120 EKGTKKKFELFVLDPAQDWYRWLFVIAAMPVLYNWCLLVARACFSDLQRYFVWLVLD 179
 QY 182 YFSDTVYIADLIIRLTGTGLEQLAVKPKLRDNYIHTLOPKLDVASIIPDLYFAVG 241
 Db 180 YFSDVVIADLFIRLTGTGLEQLAVKPKLRDNYIHTLOPKLDVASIIPDLYFAVG 239
 QY 242 IHSPEVRFNRLHFARMFEFFDRTETRTSYPNIFRISNLVLYLVIHWNACIYYVVISKS 301
 Db 240 IHNPEVRFNRLHFARMFEFFDRTETRTSYPNIFRISNLVLYLVIHWNACIYYAISK 299
 QY 302 IGFGVDTWYVNIPTDEYGLAREYIYCLYWSLTLLTTIGETPPPVKDEYLFVIFDFLI 361
 Db 300 IGFGVDTWYVNIPTDEYGLAREYIYCLYWSLTLLTTIGETPPPVKDEYLFVIFDFLI 359
 QY 362 GVLIIFATIVGNVSMISNNMATAEFAQKIDAVKHYMQFRKVKSKMEAKVWKDFYLTWN 421
 Db 360 GVLIIFATIVGNVSMISNNMATAEFAQKIDAVKHYMQFRKVKSKMEAKVWKDFYLTWN 419
 QY 422 KKTVDREVLKMLPAKRAEIAINVHLSLTKKVRIFQDWEAGLLVELVLKLRPQVSPGD 481
 Db 420 KKSVDREVLKMLPAKRAEIAINVHLSLTKKVRIFQDCEAGLLVELVLKLRPQVSPGD 479
 QY 482 YICRGDYGKEMYYIKGKLAIVADDGVTQYALLSAGSCFGEISILINIKSGKMGNRRTAN 541

Db 480 YTCRKGDIKEMYYIIKEGKLVAVDDGVTVQYALLSAGSCFGEISILNIKSGXMRRTAN 539
 QY 542 IRSLGYSDFCLSKODLMEAVTEAPDAKKVLEERGREILMKGLDENVAASMEVDVOE 601
 Db 540 IRSLGYSDFCLSKODLMEAVTEAPDAKKVLEERGREILMKGLDENVAASMEVDVOE 599
 QY 602 KLEQLETNMDTLTYTRFARLLAETGAAQOKLQKORITVLETKMKQNHDDYLSGINTPEPT 661
 Db 600 KLEQLETNMDTLTYTRFARLLAETGAAQOKLQKORITVLETKMKQNHDDYLSGINTPEPT 659
 QY 662 A 662
 Db 660 A 660

RESULT 4
 150630
 alpha subunit of cone photoreceptor CNG-channel - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999
 C:Accession: I50630
 R:Bonigk, W.; Altenhofen, W.; Muller, F.; Dose, A.; Illing, M.; Molday, R.S.; Kaupp, U.B.
 Neuron 10, 865-877, 1993
 A:Title: Rod and cone photoreceptor cells express distinct genes for cGMP-gated channels
 A:Reference number: I50630; PMID:93264082; PMID:7684234
 A:Accession: I50630
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-735 <BON>
 A:Cross-references: EMBL:X89598; NID:9908850; PIDN:CAA61757.1; PID:9908851
 C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
 F:524-648/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 63.9%; Score 2219.5; DB 2; Length 735;
 Best Local Similarity 59.4%; Pred. No. 3e-148;
 Matches 42; Conservative 93; Mismatches 113; Indels 89; Gaps 7;

QY 16 NNNHHPPP-----SIKANGKDDHFRAGS---RPOQVAADDDTSPQLQRLAEMD----- 59
 Db 5 NTOHSYPMGHGLSVRTTDEIERIENGFIHTSLC--EDTSSQLQVISMEGRHLSGSQT 62
 QY 60 TPARGGGQFQIVRLGVIRDWANKNFRPEPPDSFLERFRGPELQTVTHQG----- 113
 Db 63 SPFTGRGAMARLSRFVVSLSRWATRLHHEDQRPDSFLERIRGPELVEVSSRQSNIRSL 122
 QY 114 -----D 114
 Db 123 GIREQGGVNGPWLARFNVNFSNNTNEDKKEKVEKKEKKEKKEKKEKDDKDDK 182
 QY 115 DKGKDGEGKTKKKFELFVLDPAQDWYRWLFVIAFVLYNWCILVARACFSDLQRYN 174
 Db 183 KKDDKKDDKKKEQKEVFVIDPSSNNYNNWLTIIAAPFYNWCMILICRACFDELQIDHI 242
 QY 175 VVWLVDYFSDTVYIADLIIRLTGLEOGLLVKDPKRLDNYIHTLOKLDVASIIPTD 234
 Db 243 KWLFDYCSDIIVDFDMFVRFTGLEOGLLVKDEKLDHDTYQTQVQKLDVLSLPTD 302
 QY 235 LIYFAVGIIHSPVFRNRLHFAFMFFORTTERTSYNIFRISNLVYLTVLIHWNACI 294
 Db 303 LAYKLGLNYPFLFRNRLHFAFMFFORTTERTSYNIFRISNLVYLTVLIHWNACI 362
 QY 295 YVWISKISGVDTWYVNTDPEYGLAREYIYCLYWSLTTLTTIGETPPPVKDEYLF 354
 Db 363 YFAISKVIGFGDSWYVNVISPEYGRLSRYIYLSYWSLTTLTTIGETPPPVKDEYLF 422
 QY 355 VIEDELIGLIFATIVGNVCSMISNNATPAEQAIDAVKHQYQFRKYSKDEAKVIKW 414
 Db 423 VVDFLVGLVLIIFATIVGNVCSMISNNATPAEQAIDAVKHQYQFRKYSKDEAKVIKW 482
 QY 415 FDYLTWNTKTVDERVLKPLAKRAEIALNVHLSLTKKVRIFQDMEAGLLVVLKLRP 474
 Db 483 FDYLTWNTKTVDERVLKPLAKRAEIALNVHLSLTKKVRIFQDMEAGLLVVLKLRP 542

QY 475 QVFSFGDITCRKGDIGKEMYYIIKEGKLVAVDDGVTVQYALLSAGSCFGEISILNIKSGX 534
 Db 543 TVFSFGDITCRKGDIGKEMYYIIKEGKLVAVDDGVTVQYALLSAGSCFGEISILNIKSGX 602
 QY 535 GNRRTANIRSLGYSDFCLSKODLMEAVTEAPDAKKVLEERGREILMKGLDENVAAS 594
 Db 603 GNRRTANIRSLGYSDFCLSKODLMEAVTEAPDAKKVLEERGREILMKGLDENVAAS 662
 QY 595 ME-VVQEKLEOLEFNMDTLTYTRFARLLAETGAAQOKLQKORITVLETKMKQNHDDYLS 653
 Db 663 ADPKOLEKIDRLDLETALDTLQTRFARLLAETGAAQOKLQKORITVLETKMKQNHDDYLS 717
 QY 654 GINTPEP 660
 Db 718 SLSVGEF 724

RESULT 5
 A55251
 cyclic nucleotide-gated Ca++ channel protein CNM-3 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 13-Aug-1999
 C:Accession: A55251; S43976
 R:Biel, M.; Zong, X.; Distler, M.; Bosse, E.; Klugbauer, N.; Murakami, M.; Flockerzi, V.
 Proc. Natl. Acad. Sci. U.S.A. 91, 3505-3509, 1994
 A:Title: Another member of the cyclic nucleotide-gated channel family, expressed in tes
 A:Reference number: A55251; PMID:94224768; PMID:8170936
 A:Accession: A55251
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-706 <BIE>
 A:Cross-references: GB:X76485; NID:9488728; PIDN:CAA54023.1; PID:9488729
 A:Experimental source: kidney
 R:Weyand, I.; Godde, M.; Frings, S.; Weiner, J.; Mueller, F.; Altenhofen, W.; Hatt, H.;
 Nature 368, 859-863, 1994
 A:Title: Cloning and functional expression of a cyclic nucleotide-gated channel from me
 A:Reference number: S43976; PMID:94211295; PMID:7512693
 A:Accession: S43976
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-706 <WEY>
 A:Cross-references: GB:X89600; NID:9908823; PIDN:CAA61759.1; PID:9908824
 A:Experimental source: testis
 C:Genetics:
 A:Gene: CNM3
 C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide
 C:Keywords: cGMP binding; ion channel; ion transport; membrane protein
 F:501-625/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 61.6%; Score 2140; DB 2; Length 706;
 Best Local Similarity 60.4%; Pred. No. 1.1e-142;
 Matches 419; Conservative 94; Mismatches 119; Indels 62; Gaps 7;

QY 11 SSPANNHNNHPPPSIKANGKD--DHAGSRPQSVQVADDDTSPQLQRLAEMDTPRGRG--- 66
 Db 9 SHPTKTH-----PSVRTMDRLDCIENGSLRFLPCESTSELQEGIANET--RGLAESR 61
 QY 67 -----GFQTVRLVGVIRDWANKNFRPEPPDSFLERFRGPELQTVTHQG----- 113
 Db 62 QSSFTSQGTRLSRLSLISLWASARHLHEDQRPDSFLERFRGPELQTVTHQG----- 121
 QY 114 -----DDKGGKDG-----GKTKKKKFFELFVLD 136
 Db 122 GSQEPDPRGRSAWPLARNNTNNTCNNSKDDKAKKEKKEKKEKKEKKEKDDKDDK 181
 QY 137 PAGDWYRWLFVIAFVLYNWCILVARACFSDLQRYNFFVWLVDYFSDTVIADLIIRL 196
 Db 182 PPSNNYYIHWLTIVIAFVLYNWCILVARACFSDLQRYNFFVWLVDYFSDTVIADLIIRL 241
 QY 197 RTGLEOGLLVKDPKRLDNYIHTLOKLDVASIIPTDLIYFAVGIIHSPVFRNRLHFA 256
 Db 242 RTGLEOGLLVKDPKRLDNYIHTLOKLDVASIIPTDLIYFAVGIIHSPVFRNRLHFA 301

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QY 257 RMFEFDRTRTSYPNIRISNLVLIIVIIHWNACIYVIVSKSIGFGVDWTWVPNTID 316
Db 302 RLFEEFDRTRTNPENMERIGNLVLIIVIIHWNACIYFALSKEFTGFTDSWVPNSN 361
QY 317 PSYGLARYIYCLYVSTLTITIGTTPPPVDEEYLVFVDFLGLVLI FAFATVGNVGM 376
Db 362 PSYGLRSRYIYSLYVSTLTITIGTTPPPVDEEYLVFVDFLGLVLI FAFATVGNVGM 421
QY 377 ISNMNATRAEFQAKIDAVKHVMQFRVSKDMKAEVILKWFIDYLTWNTKKTVDREVKLPA 436
Db 422 ISNMNASRAEFQAKIDSIKOYMQFRVKTDLTRVIRWFIDYLVWANKKTVDREVKLSLD 481
QY 437 KLRAETAINVHSTLTKKVRIFQDWEAGLLVELVLKLPQVFPSPGDYICRKGDI GKEMYII 496
Db 482 KLKAEITAINVHLDTLRKVRIFQDCEAGLLVELVLKLRPAVFPSPGDYICKKGDI GKEMYII 541
QY 497 KEGKLA VADDDGTQVALLSAGSCFGEISILNTKSGKGNRRRTANIRSI GYSDLFCLSKD 556
Db 542 KEGKLA VADDDGTQVALLSAGSCFGEISILNTKSGKGNRRRTANIRSI GYSDLFCLSKD 601
QY 557 DLMEAVTEAPDAKVLLEERGREILMKWGLLDENEVAASME-VDVQEKLEBOLETNMDTLTYT 615
Db 602 DLMEAVTEAPEAKLEERGRQLMKNDLIDELAVAGADPKDIEBKVEHLETSLSLQ 661
QY 616 RFARLLAEXTGAQOKLKQRITVLETKVQKNHEDD 649
Db 662 RFARLLAEXTNATQVYKQRLSLESQVYKMGLPED 695

RESULT 6
JH0560
cyclic nucleotide-gated channel - channel catfish
C:Species: Ictalurus punctatus (channel catfish)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0560
R:Goulding, B.H.; Ngai, J.; Kramer, R.H.; Colicos, S.; Axel, R.; Siegelbaum, S.A.; Chess
Neuron 8, 45-58, 1992
A:Title: Molecular cloning and single-channel properties of the cyclic nucleotide-gated
A:Reference number: JH0560; PMID:92110008; PMID:1370374
A:Accession: JH0560
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-682 <GOU>
A:Cross-references: GB:M83111
A:Experimental source: olfactory epithelium
A:Comment: This cyclic nucleotide-gated channel is activated equally well by both cAMP and
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
C:Keywords: cAMP binding; cGMP binding; ion channel; ion transport; olfaction; transmembr
F:137-157/Domain: transmembrane #status predicted <TS1>
F:173-193/Domain: transmembrane #status predicted <TS2>
F:217-236/Domain: transmembrane #status predicted <TS3>
F:241-261/Domain: transmembrane #status predicted <TS4>
F:277-297/Domain: transmembrane #status predicted <TS5>
F:319-337/Domain: transmembrane #status predicted <TS6>
F:350-370/Domain: transmembrane #status predicted <TS6>
F:447-571/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 61.3%; Score 2131; DB 1; Length 682;
Best Local Similarity 67.7%; Pred. No. 4.6e-142;
Matches 419; Conservative 69; Mismatches 110; Indels 22; Gaps 6;

QY 34 RAGRFQSVAAADDDTSPELQRLAEMDTPR-----RGRGGFORIVRLVGVIRVDWANKNF 86
Db 28 RAESAISRDTGDDDDTSCQLQRTALELPSAEMLEAFQRRPLARLVNLVLSREWAHKS 87
QY 87 REEPRPDSFLERFRGPELQVTVTHQDDKGG--KDEGKGTKKKFELFVLDPAQWYWR 144
Db 88 VETEQRPDSEFLERFRGQ-----AANDQSAAPADAPKTKFERMEGFVVSQDIYY 140
QY 145 WLFVIAFVLYNCLLVARACFSDLQRYFVWVLVDYFSDTVVIADLIIRLTGFLQEQ 204
Db 141 WLFIALASLYNMLVARACFQDLQDENFLLWGLDYLCDVIYILDTCIRLTGFLQEQ 200
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QY 205 LLVKDPKKLRDNYIHTLQKLDVASIIPTDLIYFVAVGIHSPVFRNRLHLHARMEFEFFDR 264
Db 201 LLVKDLAKLRDNYIHTLQKLDVFSILFTELLFFVTG-YVQLRNRNRLHRSRMEFEFFDR 259
QY 265 TETRSTYPNIRISNLVLIIVIIHWNACIYVIVSKSIGFGVDWTWVPNTIDPEYGYLAR 324
Db 260 TETRSTYPNIRISNLVLIIVIIHWNACIYVIVSKSIGFGVDWTWVPNTIDPEYGYLAR 315
QY 325 EYIVCLYVSTLTITIGTTPPPVDEEYLVFVDFLGLVLI FAFATVGNVGMISNMNATR 384
Db 326 EYIVCLYVSTLTITIGTTPPPVDEEYLVFVDFLGLVLI FAFATVGNVGMISNMNATR 375
QY 385 AEFQAKIDAVKHVMQFRVSKDMKAEVILKWFIDYLTWNTKKTVDREVKLPAKRAEIAI 444
Db 376 AEFQAKIDAVKHVMQFRVSKDMKAEVILKWFIDYLTWNTKKTVDREVKLPAKRAEIAI 435
QY 445 NVHLSTLTKKVRIFQDWEAGLLVELVLKLPQVFPSPGDYICRKGDI GKEMYIIKESQLAVV 504
Db 436 NVHLSTLTKKVRIFQDWEAGLLVELVLKLPQVFPSPGDYICRKGDI GKEMYIIKESQLAVV 495
QY 505 ADDGVTQVALLSAGSCFGEISILNTKSGKGNRRRTANIRSI GYSDLFCLSKDLMVAEVT 564
Db 496 ADDGVTQVALLSAGSCFGEISILNTKSGKGNRRRTANIRSI GYSDLFCLSKDLMVAEVT 555
QY 565 APDAKVLLEERGREILMKWGLLDENEVAASMEV-DVQEKLEQLETNMDTLTYTRFARLLAB 623
Db 556 YPDAKVLLEERGREILMKWGLLDENEVAASMEV-DVQEKLEQLETNMDTLTYTRFARLLAB 615
QY 624 YTGAKQKLRITVLETKV 642
Db 616 FTSTQRLKQRITALEQL 634

RESULT 7
S74179
cyclic nucleotide-gated channel protein - human
C:Species: Homo sapiens (man)
C:Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 16-Jul-1999
C:Accession: S74179
R:Yu, W.P.; Grunwald, M.E.; Yau, K.W.
FEBS Lett. 393, 211-215, 1996
A:Title: Molecular cloning, functional expression and chromosomal localization of a hum
A:Reference number: S74179; PMID:96409310; PMID:8814292
A:Accession: S74179
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-695 <YU>
A:Experimental source: retina
C:Genetics:
C:Map position: 2
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide
C:Keywords: ion channel; ion transport; membrane protein
F:482-607/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 61.2%; Score 2126.5; DB 2; Length 695;
Best Local Similarity 61.5%; Pred. No. 9.9e-142;
Matches 429; Conservative 92; Mismatches 130; Indels 47; Gaps 11;

QY 5 KSNVGVKSPANNHHPPSIKANGKDDHRAG---SRQSVAAADDDTSPELQRLAEMDT- 60
Db 3 KINTQVSHPSRTH-----LEVTSRDLNRAENGJSRAHS---SSSETSVLPQGTAMEYR 55
QY 61 --PRGRG-----GFORIVRLVGVIRVDWANKNFRREEPRPDSFLERFRGPELQVTVTHQ 113
Db 56 GLADSGQGSFTQGIARLSRLIFLLRWAARVHHVDQGDSPDFPRFRGAELKEVSSQES 115
QY 114 D-----DKG-----GKDGKGTKKKFFELFVLDPAQWYWRLEV 148
Db 116 NQAQNVGSOEADRGSRSAWPLAKCNTNTSNTEEEKTKKK-DAIVDPSPSNLYRRLTA 174
QY 149 IAMPVLYNCLLVARACFSDLQRYFVWVLVDYFSDTVVIADLIIRLTGFLQEQGLV 208
Db 175 IALPFYFNWYLLICRACFDELOSEYIMLWLDYFSDTVVIADLIIRLTGFLQEQGLV 234
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QY 209 DPKKLRDNYIHTLOKLDVASIIPDLYIFAVGIHSPEVRENFLLHFAFMFEFFDRTETR 268
Db 235 DYNRLMQHKTQTFQKLDLSLVTDLAYLKVGTNYPEVRENFLLKFSRLFEFFDRTETR 294
QY 269 TSYPNIFRISNLVLYLIIHWNACIYVWISKISIGEGVDTWYYPNITDPEYGYLAREYIY 328
Db 295 TYNPNMERIGNLVLYLIIHWNACIYFALSKEFGSDSWYPNISIPHGRLSRKIY 354
QY 329 CLYWSLTITTTGETPPPKVDEYLFIYDFDLGLVLIIFATIVGNVSMISNNMATAEAFQ 388
Db 355 SLYWSLTITTTGETPPPKVDEYLFIYDFDLGLVLIIFATIVGNVSMISNNMATAEAFQ 414
QY 389 AKIDAVKHYMQPKVSKDMEAKVIKFDYLTWTKTVDREVLNKLPAKIRABIAINVLH 448
Db 415 AKIDSIKQYMQPKVKTDLVIRVDFYLVANKTVDEKEVLSKSPDKLKAELAINVLH 474
QY 449 STLKKVRIQDWEAGLLVELVLKLRPQVSPGDIYCRKGDIGKEMYYIKBGLAVVADGG 508
Db 475 DTLKKVRIQDCEAGLLVELVLKLRPQVSPGDIYCKKGDIGKEMYYINEGKLAVVADGG 534
QY 509 VTQYALLSAGSCFGEISILNIGSKMGNRTANIRSIGYSDLFCLSKDMLMEAVTEAP-D 567
Db 535 VTQFVLSGSGYGEISILNIGSKSGNRTANIRSIGYSDLFCLSKDMLMEALTYPGQ 594
QY 568 AKKVLREGRHILMKMGLLDENEVAASME--VDVQEKLEQLETNMDTLITRFAELLYBTG 626
Db 595 AKKALEEKGRIIMKUNLIDELARAGADPKDLKEKVEQLGSSLDITLQTFARLLAEYNA 654
QY 627 AQOKLKQRTVLTETKMKQNHEDDYLSDGINTPEPTAAE 664
Db 655 TOMMKQRLSQLESQVK-GGGDKPLADGEVPGDATKTE 691

RESULT 8
150680
alpha subunit of rod photoreceptor CNB-channel - chicken
C:Species: Gallus gallus (chicken)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999
C:Accession: I50680
R;Bonigk, W.; Alenchofen, W.; Muller, F.; Dose, A.; Illing, M.; Molday, R.S.; Kaupp, U.H.
Neuron 10, 865-877, 1993
A;Title: Rod and cone photoreceptor cells express distinct genes for cGMP-gated channels
A;Reference number: I50630; MUID:93264082; PMID:7694234
A;Accession: I50680
A;Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A;Residues: 1-645 <NON>
A;Cross-references: EMBL:X89599; NID:g908852; PIDN:CAA61758.1; PID:g908853
C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
F;431-555/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 59.5%; Score 2067; DB 2; Length 645;
Best Local Similarity 62.9%; Pred. No. 1.4e-137;
Matches 406; Conservative 78; Mismatches 123; Indels 38; Gaps 6;

QY 19 HPPPPSIKANGKODHRAGSRPQSVAAADDDTSPQLRLAEMDTPRRGRGFGQIRVLVGV 78
Db 9 HHSHPII-----PSVVVQDTSEDPGL-----IEKGNRRFARQWYLPGAF 47

QY 79 -----RDWANKNFRBEEPPDPSFLERFRGPPELQTVTHQGGDKGKGKGTKK 128
Db 48 AQYNNINNSNKDEKKKKKKSEKKNKQGERQKNEKKHKKDK-----KKGEEK 103

QY 129 KFELVLDPADGWYRMLFVIAMPVLYNWCLLVARACFSDLORNYFVVLVLDYFSDTV 188
Db 104 KQFIIDPAGMYNNLFCITLPMYNNWTMIARACFDELQNDLYLAWFWFVYVSVITY 163

QY 189 IADLIIRLTGFLQGLLVKDPKKLRDNYIHTLOKLDVASIIPDLYIFAVGIHSPEVR 248
Db 164 IADMVTRTGYLQGLLVKEEQKLKYEKSSLOKLDLSLIITDLYLFGKGLNYEPLR 223

QY 249 FNRLLHFAFMFEFFDRTETRTPSYNIFRISNLVLYLIIHWNACIYVWISKISIGFGVDT 308

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Db 224 INRLLEVARMPFFQFQFTEFTNYPNIFRISNLVLYLIIHWNACIYVWISKAIGGADT 283
QY 309 WYYPNITDPEYGYLAREYIYCYWSLTITTTGETPPPKVDEYLFIYDFDLGLVLIIFAT 368
Db 284 WYYPNITDPEYGYLAREYIYCYWSLTITTTGETPPPKVDEYLFIYDFDLGLVLIIFAT 343
QY 369 IVGNVSMISNNMATAEAFQAKIDAVKHYMQPKVSKDMEAKVIKFDYLTWTKTVDRE 428
Db 344 IVGNVSMISNNMATAEAFQAKIDAVKHYMQPKVSKDMEAKVIKFDYLTWTKTVDRE 403
QY 429 EYLNKLPKLRABIAINVLHSTLKKVRIQDWEAGLLVELVLKLRPQVSPGDIYCRKGD 488
Db 404 EYLNKLPKLRABIAINVLHSTLKKVRIQDWEAGLLVELVLKLRPQVSPGDIYCRKGD 463
QY 489 IGKEMYYINEGKLAVVADGGVTQYALLSAGSCFGEISILNIGSKMGNRTANIRSIGYS 548
Db 464 IGKEMYYINEGKLAVVADGGVTQYALLSAGSCFGEISILNIGSKMGNRTANIRSIGYS 523
QY 549 DLFCLSKDDMLMEAVTEAPDAKKVLEERGREIIMKMGLLDENEVA--ASMEVDVQEKLEQ 606
Db 524 DLFCLSKDDMLMEALTYPGADAKMLEKKGKQLMKDGLLD-IEVANLGSPPKDLKEKVAYM 582
QY 607 ETNMDTLITRFAELLYBTGAAQOKLKQRTVLTETKMKQNHEDDYL 651
Db 583 EGSMDRLQTKFARLLAEYDAAQOKLKQRTVLTETKMKQNHEDDYL 627

RESULT 9
S07103
cGMP-gated ion channel protein - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S07103
R;Kaupp, U.B.; Miodini, T.; Tanabe, T.; Terada, S.; Boenigk, W.; Stuehmer, W.; Cook, N.
Nature 342, 762-766, 1989
A;Title: Primary structure and functional expression from complementary DNA of the rod
A;Reference number: S07103; MUID:90098076; PMID:2481236
A;Accession: S07103
A;Status: not compared with conceptual translation
A:Molecule type: mRNA
A;Residues: 1-690 <NAU>
A;Cross-references: GB:X51604; NID:g203; PIDN:CAA35947.1; PID:g204
C;Note: part of this sequence was confirmed by protein sequencing
C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
C;Keywords: cGMP binding; eye; ion channel; ion transport; retina; transmembrane protei
F;477-601/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 58.8%; Score 2044; DB 1; Length 690;
Best Local Similarity 63.5%; Pred. No. 6.3e-136;
Matches 401; Conservative 82; Mismatches 118; Indels 30; Gaps 7;

QY 41 SVAADDDTSPQLRLAEMDTPRRGRGFG-----QRIVRLVGVIR--DWANKNER 87
Db 37 SPSGDDDDSGASMPSESEETNP-HARDSFRSNTHGSGSQSQREQLYLPALFNVNNSNK 95

QY 88 EEEPP-----RPDSFLERFRGPPELQTVTHQGGDKGKGKGTG--KKFELF 133
Db 96 EQEPKPKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 154

QY 134 VLDPADGWYRMLFVIAMPVLYNWCLLVARACFSDLORNYFVVLVLDYFSDTVIADLI 193
Db 155 VIDPSGNTYNNLFCITLPMYNNWTMIARACFDELQSDYLEYLAFLYLDVYVLLDMF 214

QY 194 IRLRTGFLQGLLVKDPKKLRDNYIHTLOKLDVASIIPDLYIFAVGIHSPEVRNRL 253
Db 215 VRTRTGFLQGLLVKDPKKLRDNYIHTLOKLDVASIIPDLYIFAVGIHSPEVRNRL 274

QY 254 HFARMEFFORTTRTPSYNIFRISNLVLYLIIHWNACIYVWISKISIGFGVDTWYYPN 313
Db 275 RISMEFFORTTRTPSYNIFRISNLVLYLIIHWNACIYVWISKISIGFGVDTWYYPN 334

QY 314 ITDPEYGYLAREYIYCYWSLTITTTGETPPPKVDEYLFIYDFDLGLVLIIFATIVGNV 373

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354 FVIFDFLIGVLIFATIVGNVSMISNMNATRAEFOAKIDAVKHVQFVKYSKMEAKVIK 413
377 FVVVDFLIGVLIFATIVGNVSMISNMNATRAEFOAKIDAVKHVQFVKYSKMEAKVIK 436
414 WFDYLTNKKTVDBREVLKNIIPAKLRABIAINVLSTLKKVIRIFQDWEAGLLVBLVKLR 473
437 WFDYLTNKKTVDBREVLKNIIPAKLRABIAINVLSTLKKVIRIFQDWEAGLLVBLVKLR 496
474 PQVSPGDYICRKGDIKEMIIKEGKLVAVDDGVVQYALLSAGSCFGEISILNIKSGK 533
497 PQVSPGDYICRKGDIKEMIIKEGKLVAVDDGVVQYALLSAGSCFGEISILNIKSGK 556
534 MGNRRRTANIRSLGYSDFCLSKDDLMBAVTEAPDAKVLREGRREILMKMGLLDENEV-A 592
557 AGNRRRTANIRSLGYSDFCLSKDDLMBAVTEAPDAKVLREGRREILMKMGLLDENEV-A 616
593 ASMEVDVQEKLEQLETNMDTLTYFRARLLAETGAQOKLQKRIITVLETKMKQNHEDYLS 652
617 GSDPKDLEEKVTRMEGSDVLLQTRFARILAEYESMOQKLKQRLTKVERFLKPLDITBFS 676

RESULT 12
JC6509
rod cyclic nucleotide-gated cation channel protein alpha-chain - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
C;Accession: JC6509
R;Veske, A.; Nilsson, S.E.G.; Gal, A.
Gene 202, 115-119, 1997
A;Title: Characterization of canine rod photoreceptor cGMP-gated cation channel alpha-subunit
A;Reference number: JC6509; MUID:98087425; PMID:9427553
A;Accession: JC6509
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-691 <VES>
A;Cross-references: EMBL:X99914; NID:g1488571; PIDN:CAA68186.1; PID:g1488572
C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-binding domain
F;478-602/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 58.18; Score 2017.5; DB 2; Length 691;
Best Local Similarity 61.38; Pred. No. 4.6e-134;
Matches 398; Conservative 94; Mismatches 126; Indels 31; Gaps 7;

QY 23 PSIKANGKDHRRAGSRPQSVAAAD---DTSPELQRLAEMDTPR-----RGRGQFOR 70
DB 21 PDIE---KEIRRMENGARSFSDDDGDDSDASMESENETPHARDSCRNNQSRDPSQR 77
QY 71 IVPLVGVR--DWANKNFRBEPDPSFLERFRGPELQTVTTHQGD-----DKG 117
DB 78 EOYLPGAIALFNVNNSSNKEQEPKKEKKKKKKSGDKNENKKSEKKKKKEKKEKK 137
QY 118 GKDGEGKGTG--KKFELFVLDPADGWYRWLFVIAFVPLVYNWCLLVARACFSDLQRYV 175
DB 138 NKEEGKDKKEEKKEVWVIDPAGWNYNMLFCITLFWNYNWTMIARACFDELQSDYLE 197
QY 176 VMLVLDYFSTVYIADLIIRLTGFLBQGLLVKDPKLRDNYIHTLQFKLDVASIIPD 235
DB 198 YWIIFDYLSDIVLLDMFVTRTGYLEQGLLVAREAKLIEKYSNLFQKLDVLSVPTDL 257
QY 236 IYFAVGHSPEVRNRLHFAFMFEFDRTRTSYNIFRISNLVLIIVIIHWNACIY 295
DB 258 LYFKLGWNYPEIRNLRLIRSRMFEFFQRTETRTNYNIFRISNLVMIIVIIHWNACV 317
QY 296 YVTSKSGFGVDTWVYENITDPEYGLAREYIYCLYWSTLTLTIGTPPPVKDEEYLFV 355
DB 318 FSISKALGFGNDTWVYEDVNDPEFGLARKYVLSYVSTLTLTIGTPPPVKDSEYVF 377
QY 356 IFDFLIGVLIFATIVGNVSMISNMNATRAEFOAKIDAVKHVQFVKYSKMEAKVIK 415
DB 378 VDFLIGVLIFATIVGNVSMISNMNATRAEFOAKIDAVKHVQFVKYSKMEAKVIK 437
QY 416 DYLTWNKKTVDBREVLKNIIPAKLRABIAINVLSTLKKVIRIFQDWEAGLLVBLVKLR 475

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438 DYLTWNKKTVDBREVLKNIIPAKLRABIAINVLSTLKKVIRIFQDWEAGLLVBLVKLR 497
476 VFPSPGDYICRKGDIKEMIIKEGKLVAVDDGVVQYALLSAGSCFGEISILNIKSGK 535
498 VFPSPGDYICRKGDIKEMIIKEGKLVAVDDGVVQYALLSAGSCFGEISILNIKSGK 557
536 NRRRTANIRSLGYSDFCLSKDDLMBAVTEAPDAKVLREGRREILMKMGLLDENEV-AAS 594
558 NRRRTANIRSLGYSDFCLSKDDLMBAVTEAPDAKVLREGRREILMKMGLLDENEV-AAS 617
595 MEYDVQEKLEQLETNMDTLTYFRARLLAETGAQOKLQKRIITVLETKMK 643
618 DPXDLKLEKVTMRGSDVLLQTRFARILAEYESMOQKLKQRLTKVERFLK 666

RESULT 13
B42161
cGMP-gated cation channel, rod photoreceptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 16-Jul-1999
C;Accession: B42161
R;Pittler, S.J.; Lee, A.K.; Altherr, M.R.; Howard, T.A.; Seldin, M.F.; Hurwitz, R.L.; &
J. Biol. Chem. 267, 6257-6262, 1992
A;Title: Primary structure and chromosomal localization of human and mouse rod photoreceptor cGMP-gated cation channel; cAMP receptor protein cyclic nucleotide-binding domain
A;Reference number: A42161; MUID:92210603; PMID:1372902
A;Accession: B42161
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-688 <PIT>
A;Cross-references: GB:M84742
A;Note: authors translated the codon TAT for residue 544 as Thr
C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-binding domain
F;475-599/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 57.48; Score 1995.5; DB 2; Length 688;
Best Local Similarity 61.04; Pred. No. 1.6e-132;
Matches 398; Conservative 88; Mismatches 143; Indels 23; Gaps 6;

QY 21 PPSIKANGKDHRRAGSRPQSVAAADDTSPQLRLAEMDTPRGG-----RGGFORIVRLV 75
DB 20 PNIVIPAIEKEIRRMENGARSFSDDDGDDSDASMESENETPHARDSCRNNQSRDPSQR 79
QY 76 GV-----IRDWANKN-----FREEPRPSFLERFRGPELQTVTTHQGD--DKG 119
DB 80 GTWALFNVNNSSNKEQEPKKEKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 139
QY 120 DGEKGTGKKEKLFVLDPADGWYRWLFVIAFVPLVYNWCLLVARACFSDLQRYV 179
DB 140 TKEKKEKKK--EVVVIDPSGNTYNNLFCITLFWNYNWTMIARACFDELQSDYLEWLI 198
QY 180 LDYFSTVYIADLIIRLTGFLBQGLLVKDPKLRDNYIHTLQFKLDVASIIPD 239
DB 199 FDYVSNVYIADLMFVTRTGYLEQGLLVKDRMKLIEKYSNLFQKLDVLSVPTDL 258
QY 240 VGHSPSEVRNRLHFAFMFEFDRTRTSYNIFRISNLVLIIVIIHWNACIY 299
DB 259 FGWNYPEIRNLRLIRSRMFEFFQRTETRTNYNIFRISNLVMIIVIIHWNACV 318
QY 300 KSIKSGFGVDTWVYENITDPEYGLAREYIYCLYWSTLTLTIGTPPPVKDEEYLFV 359
DB 319 KALGFGNDTWVYEDVNDPEFGLARKYVLSYVSTLTLTIGTPPPVKDSEYVF 378
QY 360 LIQVLIFATIVGNVSMISNMNATRAEFOAKIDAVKHVQFVKYSKMEAKVIK 419
DB 379 LIQVLIFATIVGNVSMISNMNATRAEFOAKIDAVKHVQFVKYSKMEAKVIK 438
QY 420 TNKTKTVDBREVLKNIIPAKLRABIAINVLSTLKKVIRIFQDWEAGLLVBLVKLR 479
DB 439 TNKTKTVDBREVLKNIIPAKLRABIAINVLSTLKKVIRIFQDWEAGLLVBLVKLR 498
QY 480 GDYICRKGDIKEMIIKEGKLVAVDDGVVQYALLSAGSCFGEISILNIKSGK 539

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Db 499 GYICKKGGIGREMYIIKEGLAVAVADDGTFQVWLSGSGYFGEISILNKGSKAGNRRT 558
QY 540 ANIRSGYSLDFCLSKDDLMVATEAPDAKKVLEERGRILLMKWGLLDENEV-AASMEVD 598
Db 559 ANIKSGYSLDFCLSKDDLMVATEPDAKTMLEERGRQLMKDGLLDINIAMGSDPKD 618
QY 599 VQPKLEQLETMTLTFRFARLAEYTGAAQKLKQRTITVLETKMKQNHEDDY 650
Db 619 LBEKVRMEGVSLLQTRFACILAEYESMQOKLKQRLTKVEKFLKPIETEF 670
RESULT 14
I59327
Olfactory cyclic nucleotide gated cation channel - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 31-Mar-2000
C:Accession: I59327, I58165
R:Bradley, J.; Li, J.; Davidson, N.; Lester, H.A.; Zinn, K.
Proc. Natl. Acad. Sci. U.S.A. 91, 8890-8894, 1994
A:Title: Heteromeric olfactory cyclic nucleotide-gated channels: A new subunit that conf
A:Reference number: I59327; MUID:94377458; PMID:7522325
A:Accession: I59327
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-575 <RES>
A:Cross-references: EMBL:U12623; NID:G538128; PIDN:AAA21464.1; PID:G538129
R:Limán, B.R.; Buck, L.B.
Neuron 13, 641-621, 1994
A:Title: A second subunit of the olfactory cyclic nucleotide-gated channel confers high
A:Reference number: I58165; MUID:95000663; PMID:7522482
A:Accession: I58165
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-575 <RE2>
A:Cross-references: EMBL:U12425; NID:G548083; PIDN:AAA64748.1; PID:G548084
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
F:348-472/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>
Query Match 43.7%; Score 1518; DB 2; Length 575;
Best Local Similarity 53.8%; Pred. No. 5.3e-99;
Matches 290; Conservative 101; Mismatches 142; Indels 6; Gaps 2;
QY 126 TKKKFELVLDPAQDGYVYRWLFVAMPVLYNWCLLVARACFSQLOQNYFVWLVLDYFSD 185
Db 18 TRARKLPVLDPSGDYIYNWLTMTVPFIMYNLLIVVCRACFPDLOHSLYVWAFVLDYTS 77
QY 186 TVYIADLIIRLTGFEQGLLVKDPKKLRDNYHTLQKLDVASIIPDLYFAVGHSP 245
Db 78 LLYLLDVGVRFHGFEQGLLVVDKGMASRYRTWSFLDLASLVPDAAVYVQLGPHIP 137
QY 246 EVFNRLLHFAEFDFDRTETRTSYNPFRISNLVLYILVLIHWNACIYYVSKSIGFG 305
Db 138 TLRLNRFRLVRPFEAFDRTEATAYENAPRIAKMLIXYFVVIHWNACIYFALSRYLGF 197
QY 306 VDTWVYNTDPSYGLAREYIYCLYWSLTTLTIGETPPVVDDEYLFVIFDPLGLVLI 365
Db 198 RDWVTPDPAQPFERLRQYLSYFSFTSLITLTGDTPLPDEEYLFVWVGDFLLAVMG 257
QY 366 FATVGVNVSIMNMTATRAEFOAKIDAVKHVMQFRKVKSDMEAKVIMKFDYLTWTKTV 425
Db 258 FATIMSGSSVIYNNMTADAAFPDHALVKYVKLQHVKNRLERRVIDWVQHLQINKKMT 317
QY 426 DERVLKNLPKARAEIATNVHSLTKKVRIFODWEAGLLVLEVLKLRPQVFGDYICR 485
Db 318 NEVAAILQHLPERLRAEVAVSVHLSLRVQFQCEASLLEELVLLKLPQCTYSPGEYVCR 377
QY 486 KGDIGKEMYIIKEGLAVAVDDGVTQYALLSAGSCGEISILNKGSKGNRRNTAIRSL 545
Db 378 KGDIGREMYIIRREGQAVAVDDGVTQYAVLAGLYFGEISIIINIKGNSGNRRNTAIRSL 437
QY 546 GYSDFCLSKDDLMVATEAPDAKKVLEERGRILLMKWGLLDENEVAASMEVDVQE- 601

Db 438 GYSDFCLSKDDLMVSEYPOAQVMEKRGREILLKMNKLDVNAEAA--ETALQEAATES 495
QY 602 KLEQLETNMDTYLTFARLLAEYTGAAQOKLAKORITVLETKMKQNHEDDYLSDGINTPEP 660
Db 496 RLKGLQDDLDQTRFARLLAELESSALKIAYIRLERLEWQTRFWPMPMDGEADDEAP 554
RESULT 15
S52072
DmCNGC protein - fruit fly (Drosophila sp.)
C:Species: Drosophila sp.
C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 16-Jul-1999
C:Accession: S52072
R:Baumann, A.; Frings, S.; Godde, M.; Seifert, R.; Kaupp, U.B.
EMBO J. 13, 5040-5050, 1994
A:Title: Primary structure and functional expression of a Drosophila cyclic nucleotide-
A:Reference number: S52072; MUID:95045396; PMID:7957070
A:Accession: S52072
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-665 <BAU>
C:Genetics:
A:Gene: FlyBase:Cng
A:Cross-references: FlyBase:FBgn0014462
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide
F:429-553/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>
Query Match 42.8%; Score 1487; DB 2; Length 665;
Best Local Similarity 52.3%; Pred. No. 9.9e-97;
Matches 299; Conservative 83; Mismatches 164; Indels 26; Gaps 6;
QY 87 REEPRPDSFLERFRGPELQVTTHQGDGK-----KDGEGKGTKKKPELFVLDP 138
Db 50 RNRKPPDPWFLEKFSN-----TTNTDKIRKCPAMEDAALSSEIRGSSVLCNRLSVDPT 103
QY 139 GMYRWLFIAMPVLYNWCLLVARACFSQLOQNYFVWLVLDYSDTYVIADLIIRLT 198
Db 104 LOSHYRWLAIVSLAVLYNIIFVVGRAVFEINKSAPAFWYTLDYLCDFIYLLDTLVHME 163
QY 199 GFLEQGLVVKDPKKLRDNYHTLQKLDVASIIPDLYF-----AVGIHSP---EVRF 249
Db 164 GFLEQGLVVDRAFLRRHYFTKGYLWLDVLPDLYAWPPETCSSXILPCPVIVKL 223
QY 250 NELLHFAEFDFDRTETRTSYNPFRISNLVLYILVLIHWNACIYYVSKSIGFGVDTW 309
Db 224 NELLRLNWFDFDRTETATGYENAFRIKCVVLAILVLIHWNACMYFALSIEIGFSSDSW 283
QY 310 VTPNTDPSYGLAREYIYCLYWSLTTLTIGETPPVVDDEYLFVIFDPLGLVLI 369
Db 284 VY-NLNGTRNNLTQRYISFYWSLTTLTIGETPPENDVBYLFVADFLAGVLIFATI 342
QY 370 VGVNVSIMNMTATRAEFOAKIDAVKHVMQFRKVKSDMEAKVIMKFDYLTWTKTVDERE 429
Db 343 VGNISGSMINMNVARVEFQNRMDGVKQYMAFRVGHLEARVIRWFATYWSQSGALDEER 402
QY 430 VLKNUPAKLRAEIAINVHSLTKKVRIFODWEAGLLVLEVLKLRPQVSPGYICRKGDI 489
Db 403 VLAALPDKLKABIAIQVHMDTLKQVRIPTHDTPEGLLEALVLKLVQVSPGYICRKGDI 462
QY 490 GKEMYIIKEGLAVAVDDGVTQYALLSAGSCGEISILNKGSKGNRRNTAIRSLGYS 549
Db 463 GKEMYIVRKGGLVVGDDGIVTLATLGAGSVFGEVLEIAGNRTGNRTARTANVRSILGYS 522
QY 550 LFCLSKDDLMVATEAPDAKKVLEERGRILLMKWGLLDENEVAASMEV--DVQEKLEQLE 607
Db 523 LFCLAKRDLWELSDYPEARSTLTORGCOLLRKDKGLLDEQITFADSORVHDSIEGGIEKLE 582
QY 608 TNDTYLTFARLLAEYTGAAQOKLAKORITVLE 639
Db 583 LSVENLNLRLAEYATASQAKIKQLAKLE 614
Search completed: May 12, 2004, 11:15:45

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 12, 2004, 11:07:14 ; Search time 60 Seconds
(without alignments)
3126.859 Million cell updates/sec

Title: US-10-087-217A-8

Perfect score: 3475

Sequence: 1 MWTEKSNVGVKSPANNHH.....NHEDDYLSDGINTPEPTAAE 664

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 29Jan04: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3475	100.0	664	6 AAE37222	Aae37222 Rat CNG c
2	3469	99.8	664	6 AAE37221	Aae37221 Rat CNG c
3	3456	99.5	664	6 AAE37224	Aae37224 Rat CNG c
4	3455	99.4	664	6 AAE37220	Aae37220 Rat CNG c
5	3455	99.4	664	6 AAE37223	Aae37223 Rat CNG c
6	3449	99.3	664	5 AAG79529	Aag79529 Rat HBMYC
7	3449	99.3	664	6 AAE37219	Aae37219 Rat CNG c
8	3384	97.4	664	5 AAG79528	Aag79528 Mouse HBMYC
9	3231.5	93.0	732	5 AAG79526	Aag79526 Rabbit HB
10	3204.5	92.2	663	5 AAG79527	Aag79527 Cow HBMYC
11	3204.5	92.2	663	6 ABG74912	Abg74912 Bovine CN
12	3199.5	92.1	663	6 ABG74914	Abg74914 Bovine CN
13	3198.5	92.0	663	6 ABG74913	Abg74913 Bovine CN
14	3197.5	92.0	664	4 AAE04894	Aae04894 Human tra
15	3197.5	92.0	664	5 ABB78066	Abb78066 Amino aci
16	3197.5	92.0	664	6 ABG72530	Abg72530 Novel hum
17	3197.5	92.0	664	6 ABG72529	Abg72529 Novel hum
18	3197.5	92.0	664	6 ABUI12049	Abui12049 Human NOV
19	3197.5	92.0	664	6 ABP98475	Abp98475 Amino aci
20	3184.5	91.6	664	5 AAG79525	Aag79525 Variant H
21	3179.5	91.5	664	5 AAG79524	Aag79524 HBMYCNG.
22	2139	61.6	694	5 AAE15987	Aae15987 Human CNG
23	2139	61.6	694	7 AAE38591	Aae38591 Human CNG
24	2034	58.5	686	7 ADD48640	Add48640 Human Pro
25	2030	58.4	690	7 ADD93244	Add93244 Cyclic nu

26	2028	58.4	690	5	AAE15988	Aae15988 Human CNG
27	2026	58.3	683	7	ADD48638	Add48638 Rat Prote
28	1545	44.5	575	5	ABP69252	Abp69252 Human pol
29	1545	44.5	575	5	AAE20959	Aae20959 Human tra
30	1545	44.5	575	5	ABU07725	Abu07725 Human cyc
31	1545	44.5	575	6	ABU09091	Abu09091 Human tra
32	1545	44.5	575	6	ABP55141	Abp55141 Human cyc
33	1544	44.4	568	6	ABP55142	Abp55142 Human cyc
34	1543	44.4	575	6	ABU09778	Abu09778 Human tra
35	1540	44.3	575	5	AAO14138	Aao14138 Human tra
36	1540	44.3	575	5	AAW47673	Aaw47673 MOL10b pr
37	1529	44.0	578	5	AAW47672	Aaw47672 MOL10a pr
38	1494	43.0	665	4	ABB63493	Abb63493 Drosophil
39	1185	34.1	239	6	ABP98582	Abp98582 Amino aci
40	1166	33.6	239	6	ABR39397	Abt39397 Amino aci
41	1129	32.5	702	4	ABB65859	Abb65859 Drosophil
42	1057.5	30.4	1704	6	ABU09092	Abu09092 Rat trans
43	989.5	28.5	1693	4	ABB64282	Abb64282 Drosophil
44	870.5	25.1	1037	4	ABB66545	Abb66545 Drosophil
45	825	23.7	259	4	ABG27071	Abg27071 Novel hum

ALIGNMENTS

RESULT 1

AAE37222
ID AAE37222 standard; protein; 664 AA.

XX AAE37222;

AC AAE37222;

DT 07-AUG-2003 (first entry)

DE Rat CNG channel alpha subunit mutant (C460W+Y565A+E583W).

XX Rat; G protein-coupled receptor; cyclic nucleotide-gated channel; GPCR;

KW cyclic nucleotide-gated channel; CNG channel; mutant; mutuin.

OS Rattus norvegicus.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 460

FT Misc-difference 565 /note= "Wild type Cys substituted with Trp"

FT Misc-difference 583 /note= "Wild type Tyr substituted with Ala"

FT Misc-difference 583 /note= "Wild type Glu substituted with Met"

XX WO2003038039-A2.

PD 08-MAY-2003.

XX 25-OCT-2002; 2002WO-US034122.

PR 26-OCT-2001; 2001US-0330663P.

PR 04-MAR-2002; 2002US-00087217.

XX (APTU-) APTUS PHARM INC.

XX Yao Y, Cao L;

XX WPI; 2003-430510/40.

XX N-PSDB; AAD56242.

XX New host cell comprising first and second nucleic acids with promoters that encode exogenous G protein-coupled receptor and cyclic nucleotide-gated channel, respectively, useful for identifying agents that modulate GPCR activity.

PS Claim 13; Page 95-98; 98pp; English.

XX The invention relates to compositions and methods for identifying G

CC protein-coupled receptor (GPCR), ligands and compounds that modulate GPCR
 CC-mediated activities. The invention also provides an host cell comprising
 CC first and second nucleic acids with promoters that encode exogenous G
 CC protein-coupled receptor and cyclic nucleotide-gated (CNG) channel
 CC respectively. The host cells are useful for identifying agents that
 CC modulate an activity mediated by a GPCR. The present sequence is rat CNG
 CC channel alpha subunit mutant
 XX
 SQ Sequence 664 AA;

Query Match 100.0%; Score 3475; DB 6; Length 664;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 664; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMTKSNVGVKSSPANNHHPSPSIKANGKDDHRRAGSRPQSVAAADDDTSPELQRLAEMDT 60
 DB 1 MMTKSNVGVKSSPANNHHPSPSIKANGKDDHRRAGSRPQSVAAADDDTSPELQRLAEMDT 60
 QY 61 PRGRGGFQRIIVLGVIRDWANKNFRPEEPDPSFLERFRGPELQTVTHQDGDGKGD 120
 DB 61 PRGRGGFQRIIVLGVIRDWANKNFRPEEPDPSFLERFRGPELQTVTHQDGDGKGD 120
 QY 121 GEGKGTKKPELFLVLDPAWDYRMLFVIAMPVLYNWCLLVARACFSDLQRYFVWLV 180
 DB 121 GEGKGTKKPELFLVLDPAWDYRMLFVIAMPVLYNWCLLVARACFSDLQRYFVWLV 180
 QY 181 DYFSDTVYIADLIIRLTGFLQGLLVKDPKLRDNVYHTLQKLDVASIIPDLYFAV 240
 DB 181 DYFSDTVYIADLIIRLTGFLQGLLVKDPKLRDNVYHTLQKLDVASIIPDLYFAV 240
 QY 241 GIHSPEVRNRLHFAFMPEFFDRTETRTSYNIFRISNLVLYIIVHNACIYVVISK 300
 DB 241 GIHSPEVRNRLHFAFMPEFFDRTETRTSYNIFRISNLVLYIIVHNACIYVVISK 300
 QY 301 SIGFGVDTWVYNIITDPEYGLAREYIYCLYVSTLTITTTIGETPPPVKDEEYLFVIFDEL 360
 DB 301 SIGFGVDTWVYNIITDPEYGLAREYIYCLYVSTLTITTTIGETPPPVKDEEYLFVIFDEL 360
 QY 361 NIRSGLGSDYLCISKDDLMEAVTEAPDAKKVLEERGREILMKMGLLDENEVAASMEVDVQ 600
 DB 361 NIRSGLGSDYLCISKDDLMEAVTEAPDAKKVLEERGREILMKMGLLDENEVAASMEVDVQ 600
 QY 601 EKLEQETNMDITYRFARLAETGAQOKLQKRIITVLETMKQNHDDYLSGINTPEP 660
 DB 601 EKLEQETNMDITYRFARLAETGAQOKLQKRIITVLETMKQNHDDYLSGINTPEP 660
 QY 661 TAAE 664
 DB 661 TAAE 664

RESULT 2

AAE37221

ID AAE37221 standard; protein; 664 AA.

XX

AC AAE37221;

XX

DT 07-AUG-2003 (first entry)

XX

DE Rat CNG channel alpha subunit mutant.

XX

KW Rat; G protein-coupled receptor; cyclic nucleotide-gated channel; GPCR;
 KW cyclic nucleotide-gated channel; CNG channel; mutant; mutein.

OS Rattus norvegicus.
 OS Synthetic.

PN WO2003038039-A2.

XX

PD 08-MAY-2003.

XX

PF 25-OCT-2002; 2002WO-US034122.

XX

PR 26-OCT-2001; 2001US-0330663P.

PR

PR 04-MAR-2002; 2002US-00087217.

XX

PA (APTU-) APTUS PHARM INC.

PI

PI Yao Y, Cao L;

DR

DR WPI; 2003-430510/40.

DR

DR N-PSDB; AAD56241.

XX

PT New host cell comprising first and second nucleic acids with promoters
 PT that encode exogenous G protein-coupled receptor and cyclic nucleotide-
 PT gated channel, respectively, useful for identifying agents that modulate
 PT GPCR activity.

PS

PS Claim 13; Page 89-92; 98pp; English.

XX

CC The invention relates to compositions and methods for identifying G
 CC protein-coupled receptor (GPCR), ligands and compounds that modulate GPCR
 CC-mediated activities. The invention also provides an host cell comprising
 CC first and second nucleic acids with promoters that encode exogenous G
 CC protein-coupled receptor and cyclic nucleotide-gated (CNG) channel
 CC respectively. The host cells are useful for identifying agents that
 CC modulate an activity mediated by a GPCR. The present sequence is rat CNG
 CC channel alpha subunit mutant

XX

SQ Sequence 664 AA;

Query Match 99.8%; Score 3469; DB 6; Length 664;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 663; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MMTKSNVGVKSSPANNHHPSPSIKANGKDDHRRAGSRPQSVAAADDDTSPELQRLAEMDT 60

DB 1 MMTKSNVGVKSSPANNHHPSPSIKANGKDDHRRAGSRPQSVAAADDDTSPELQRLAEMDT 60

QY 61 PRGRGGFQRIIVLGVIRDWANKNFRPEEPDPSFLERFRGPELQTVTHQDGDGKGD 120

DB 61 PRGRGGFQRIIVLGVIRDWANKNFRPEEPDPSFLERFRGPELQTVTHQDGDGKGD 120

QY 121 GEGKGTKKPELFLVLDPAWDYRMLFVIAMPVLYNWCLLVARACFSDLQRYFVWLV 180

DB 121 GEGKGTKKPELFLVLDPAWDYRMLFVIAMPVLYNWCLLVARACFSDLQRYFVWLV 180

QY 181 DYFSDTVYIADLIIRLTGFLQGLLVKDPKLRDNVYHTLQKLDVASIIPDLYFAV 240

DB 181 DYFSDTVYIADLIIRLTGFLQGLLVKDPKLRDNVYHTLQKLDVASIIPDLYFAV 240

QY 241 GIHSPEVRNRLHFAFMPEFFDRTETRTSYNIFRISNLVLYIIVHNACIYVVISK 300

DB 241 GIHSPEVRNRLHFAFMPEFFDRTETRTSYNIFRISNLVLYIIVHNACIYVVISK 300

QY 301 SIGFGVDTWVYNIITDPEYGLAREYIYCLYVSTLTITTTIGETPPPVKDEEYLFVIFDEL 360

DB 301 SIGFGVDTWVYNIITDPEYGLAREYIYCLYVSTLTITTTIGETPPPVKDEEYLFVIFDEL 360

QY 361 IGVLIFATIVGVNVMISNNATRAEFQAKIDAVKHVMQFRKVSQDMEAKVVKFDFLWT 420

DB 361 IGVLIFATIVGVNVMISNNATRAEFQAKIDAVKHVMQFRKVSQDMEAKVVKFDFLWT 420

QY 421 NKKTVDEREVLKMLPAKLRAEIAINVHLSTLKKVRIQDWEAGLLVELVLKLRPQVFSFG 480

```

Db 421 NKKTVDEREVLKPAKLAETAINVHLSTLKKVRFQDWEAGLLVELVLRPQVFSFG 480
QY 481 DYICRKGDIGKEMYYIKKGLAVVADGGVTOVALLSAGSCFGEISILINIKGSKGNRRTA 540
Db 481 DYICRKGDIGKEMYYIKKGLAVVADGGVTOVALLSAGSCFGEISILINIKGSKGNRRTA 540
QY 541 NIRSGLYDLFCLSKDDLMKGLDENEVAASMEVDVQ 600
Db 541 NIRSGLYDLFCLSKDDLMKGLDENEVAASMEVDVQ 600
QY 601 EKLEQLETNMDTLTYTRFARLLABYTGAQOKLKORITVLETKMKQNHDDYLSGINTPEP 660
Db 601 EKLEQLETNMDTLTYTRFARLLABYTGAQOKLKORITVLETKMKQNHDDYLSGINTPEP 660
QY 661 TAAE 664
Db 661 TAAE 664

RESULT 3
AAE37224
ID AAE37224 standard; protein; 664 AA.
XX
AC AAE37224;
XX
XX 07-AUG-2003 (first entry)
XX
XX Rat CNG channel alpha subunit mutant (C460H+E583W).
XX
XX Rat; G protein-coupled receptor; cyclic nucleotide-gated channel; GPCR;
XX KW cyclic nucleotide-gated channel; CNG channel; mutant; mutein.
XX
XX Rattus norvegicus.
XX OS Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 460
FT /note= "Wild type Cys substituted with His"
FT Misc-difference 583
FT /note= "Wild type Glu substituted with Met"
XX
XX WO2003038039-A2.
XX
XX 08-MAY-2003.
XX
XX 25-OCT-2002; 2002WO-US034122.
XX
XX 26-OCT-2001; 2001US-0330663P.
XX PR 04-MAR-2002; 2002US-00087217.
XX
XX (APTU-) APTUS PHARM INC.
XX
XX Yao Y, Cao L;
XX WPI; 2003-430510/40.
XX
XX New host cell comprising first and second nucleic acids with promoters
XX PT that encode exogenous G protein-coupled receptor and cyclic nucleotide-
XX PT gated channel, respectively, useful for identifying agents that modulate
XX PT GPCR activity.
XX
XX Example 10; Page; 98pp; English.
XX
XX The invention relates to compositions and methods for identifying G
XX CC protein-coupled receptor (GPCR), ligands and compounds that modulate GPCR
XX CC protein-coupled activities. The invention also provides an host cell comprising
XX CC first and second nucleic acids with promoters that encode exogenous G
XX CC protein-coupled receptor and cyclic nucleotide-gated (CNG) channel
XX CC respectively. The host cells are useful for identifying agents that
XX CC modulate an activity mediated by a GPCR. The present sequence is rat CNG
XX CC channel alpha subunit mutant. Note: This sequence is not shown in the
XX CC specification but is derived from the rat CNG channel alpha subunit wild-

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CC type protein shown as SEQ ID NO: 2 (AAE37219) in page 78-80 of the
CC specification
XX
SQ Sequence 664 AA;
Query Match 99.5%; Score 3456; DB 6; Length 664;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 662; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MMTESKNGVKSPANNHHPPPSIKANKGDHRRAGSRPQSVAAADDTSPELORLAEMDT 60
Db 1 MMTESKNGVKSPANNHHPPPSIKANKGDHRRAGSRPQSVAAADDTSPELORLAEMDT 60
QY 61 PRGRGGGFORIVRLGVIRDMANKKFRFEEPRPDSFLERFRGPELQTVTTHQDDKGGKD 120
Db 61 PRGRGGGFORIVRLGVIRDMANKKFRFEEPRPDSFLERFRGPELQTVTTHQDDKGGKD 120
QY 121 GEGKTKKKFELFVLDPAGDWTYRWLFVIAMPVLYNWCILVARACFSDLQRNYFVWVLVL 180
Db 121 GEGKTKKKFELFVLDPAGDWTYRWLFVIAMPVLYNWCILVARACFSDLQRNYFVWVLVL 180
QY 181 DYFSDTVVIADLIIRLTGTFLEQGLLVKDPKKLRDNYIHTLOFKLDVASIIPDLYFAV 240
Db 181 DYFSDTVVIADLIIRLTGTFLEQGLLVKDPKKLRDNYIHTLOFKLDVASIIPDLYFAV 240
QY 241 GIHSPVRENRLLHFARMEFFEDRTETRTSYNIFRISNLVLYLIIHWNACIYVVISK 300
Db 241 GIHSPVRENRLLHFARMEFFEDRTETRTSYNIFRISNLVLYLIIHWNACIYVVISK 300
QY 301 SIGFGVDTWVYNIITDPEYGLAREYIYCLYKSTLTLTITGETPPPVKDEEYLFVIFDEL 360
Db 301 SIGFGVDTWVYNIITDPEYGLAREYIYCLYKSTLTLTITGETPPPVKDEEYLFVIFDEL 360
QY 361 IGVLIPTATVGNVSGMISNMNATRAEFQAKIDAVKHVMQFRKVSQDMEAKVIKWFYLT 420
Db 361 IGVLIPTATVGNVSGMISNMNATRAEFQAKIDAVKHVMQFRKVSQDMEAKVIKWFYLT 420
QY 421 NKKTVDEREVLKPAKLAETAINVHLSTLKKVRFQDWEAGLLVELVLRPQVFSFG 480
Db 421 NKKTVDEREVLKPAKLAETAINVHLSTLKKVRFQDWEAGLLVELVLRPQVFSFG 480
QY 481 DYICRKGDIGKEMYYIKKGLAVVADGGVTOVALLSAGSCFGEISILINIKGSKGNRRTA 540
Db 481 DYICRKGDIGKEMYYIKKGLAVVADGGVTOVALLSAGSCFGEISILINIKGSKGNRRTA 540
QY 541 NIRSGLYDLFCLSKDDLMKGLDENEVAASMEVDVQ 600
Db 541 NIRSGLYDLFCLSKDDLMKGLDENEVAASMEVDVQ 600
QY 601 EKLEQLETNMDTLTYTRFARLLABYTGAQOKLKORITVLETKMKQNHDDYLSGINTPEP 660
Db 601 EKLEQLETNMDTLTYTRFARLLABYTGAQOKLKORITVLETKMKQNHDDYLSGINTPEP 660
QY 661 TAAE 664
Db 661 TAAE 664

RESULT 4
AAE37220
ID AAE37220 standard; protein; 664 AA.
XX
XX AAE37220;
XX
XX 07-AUG-2003 (first entry)
XX
XX Rat CNG channel alpha subunit mutant (Y565A).
XX DE Rat; G protein-coupled receptor; cyclic nucleotide-gated channel; GPCR;
XX KW cyclic nucleotide-gated channel; CNG channel; mutant; mutein.
XX OS Rattus norvegicus.
XX OS Synthetic.

```



```

CC specification
XX SQ Sequence 664 AA;
    Query Match      99.4%; Score 3455; DB 6; Length 664;
    Best Local Similarity 99.7%; Pred. No. 0;
    Matches 662; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MMTEKSGVKSPPANNHHPPPSIKANGKDDHRAGSRPOSVAADDDTSPQLRLAEMDT 60
DB 1 MMTEKSGVKSPPANNHHPPPSIKANGKDDHRAGSRPOSVAADDDTSPQLRLAEMDT 60
QY 61 PRGRGGFQRIVLGVIRDMANKNPREPRDPSFLERPRGPELQVTVTHQDGGKGD 120
DB 61 PRGRGGFQRIVLGVIRDMANKNPREPRDPSFLERPRGPELQVTVTHQDGGKGD 120
QY 121 GEGKGTKKKFFELFVLDPAQDWYRWLFVIAIMPVLYNWCLLVARACFSDLQRYFVWLV 180
DB 121 GEGKGTKKKFFELFVLDPAQDWYRWLFVIAIMPVLYNWCLLVARACFSDLQRYFVWLV 180
QY 181 DYFSDTVYIADLIIRLTGTGLEQGLLVKDPKCLRDNYIHTLQPKLDVASIIPDLYFV 240
DB 181 DYFSDTVYIADLIIRLTGTGLEQGLLVKDPKCLRDNYIHTLQPKLDVASIIPDLYFV 240
QY 241 GIHSPVRENRLHFAHMFEPDRTETSYNIFRISNLVLYLVIHWNACIYYVISK 300
DB 241 GIHSPVRENRLHFAHMFEPDRTETSYNIFRISNLVLYLVIHWNACIYYVISK 300
QY 301 SIGFGVDTWVYPNITDPEYGLAREYIYCLYWSLTLTITIGETPPPVKDEYLFVIFDL 360
DB 301 SIGFGVDTWVYPNITDPEYGLAREYIYCLYWSLTLTITIGETPPPVKDEYLFVIFDL 360
QY 361 IGVLIIFATIVGNVGSMSNNATRAEFQAKIDAVKHVMQFRKYSKOMEAKVIKWFYLT 420
DB 361 IGVLIIFATIVGNVGSMSNNATRAEFQAKIDAVKHVMQFRKYSKOMEAKVIKWFYLT 420
QY 421 NKKTVDEREVLKPLPAKLRAEIAINVHLSLTKKVRIFQDWEAGLLVELVLKLRPQVSPG 480
DB 421 NKKTVDEREVLKPLPAKLRAEIAINVHLSLTKKVRIFQDWEAGLLVELVLKLRPQVSPG 480
QY 481 DYICRKGDIKEMYYIIKEGKLVAVDDGVTQYALLSAGSCFGEISILNKGSKGNRRTA 540
DB 481 DYICRKGDIKEMYYIIKEGKLVAVDDGVTQYALLSAGSCFGEISILNKGSKGNRRTA 540
QY 541 NIRSLSGSDLCFSLKODLMEAVTEAPDAKKVLEERGREIILMKGLLDENEVAASMEYDVQ 600
DB 541 NIRSLSGSDLCFSLKODLMEAVTEAPDAKKVLEERGREIILMKGLLDENEVAASMEYDVQ 600
QY 601 EKLEQLETNMDTLYTRFARLLAEYTGAAQOKIKORITVLETKMKQNHEDDYLSDGINTPEP 660
DB 601 EKLEQLETNMDTLYTRFARLLAEYTGAAQOKIKORITVLETKMKQNHEDDYLSDGINTPEP 660
QY 661 TAAB 664
DB 661 TAAB 664
RESULT 6
AAG79529
ID AAG79529 standard; protein; 664 AA.
XX AC AAG79529;
XX DT 09-DEC-2002 (first entry)
XX DE Rat HBMYCNG.
XX KW Human; cation channel; cyclic nucleotide gated; HBMYCNG;
XX KW ion channel-related disorder; stroke; depression; liver disease;
XX KW Alzheimer's disease; Parkinson's disease; arrhythmia; diabetes;
XX KW chronic pain; hypercalcaemia; hypocalcaemia; hypercalciuria; anxiety;
XX KW hypocalciuria; gastrointestinal disorder; renal disease.
OS Rattus norvegicus.
XX PN WO200268471-A2.
XX PD 06-SEP-2002.
XX PF 21-DEC-2001; 2001WO-US050413.
XX PR 21-DEC-2000; 2000US-0257865P.
XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX PI Feder J, Mintier G, Ramanathan C, Westphal R;
XX DR WPI; 2002-691655/74.
XX PT New human HBMYCNG genes, useful for treating ion channel-related
XX PT disorders e.g. stroke, anxiety and depression, Alzheimer's or Parkinson's
XX PT disease, diabetes or arrhythmia.
XX PS Disclosure; Fig 4; 177pp; English.
XX CC The sequences given in AAG79526-29 represent rabbit, cow, mouse and rat
XX CC versions of the human cation channel polypeptide designated HBMYCNG.
XX CC HBMYCNG is a human cyclic nucleotide gated cation channel with six
XX CC transmembrane domains. HBMYCNG genes are useful for treating ion channel-
XX CC related disorders, e.g. stroke, anxiety and depression, Alzheimer's or
XX CC Parkinson's disease, arrhythmia, diabetes, chronic pain, hypercalcaemia,
XX CC hypocalcaemia, hypercalciuria, hypocalciuria, gastrointestinal disorders,
XX CC ion disorders or renal or liver disease
XX SQ Sequence 664 AA;
    Query Match      99.3%; Score 3449; DB 5; Length 664;
    Best Local Similarity 99.5%; Pred. No. 0;
    Matches 661; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MMTEKSGVKSPPANNHHPPPSIKANGKDDHRAGSRPOSVAADDDTSPQLRLAEMDT 60
DB 1 MMTEKSGVKSPPANNHHPPPSIKANGKDDHRAGSRPOSVAADDDTSPQLRLAEMDT 60
QY 61 PRGRGGFQRIVLGVIRDMANKNPREPRDPSFLERPRGPELQVTVTHQDGGKGD 120
DB 61 PRGRGGFQRIVLGVIRDMANKNPREPRDPSFLERPRGPELQVTVTHQDGGKGD 120
QY 121 GEGKGTKKKFFELFVLDPAQDWYRWLFVIAIMPVLYNWCLLVARACFSDLQRYFVWLV 180
DB 121 GEGKGTKKKFFELFVLDPAQDWYRWLFVIAIMPVLYNWCLLVARACFSDLQRYFVWLV 180
QY 181 DYFSDTVYIADLIIRLTGTGLEQGLLVKDPKCLRDNYIHTLQPKLDVASIIPDLYFV 240
DB 181 DYFSDTVYIADLIIRLTGTGLEQGLLVKDPKCLRDNYIHTLQPKLDVASIIPDLYFV 240
QY 241 GIHSPVRENRLHFAHMFEPDRTETSYNIFRISNLVLYLVIHWNACIYYVISK 300
DB 241 GIHSPVRENRLHFAHMFEPDRTETSYNIFRISNLVLYLVIHWNACIYYVISK 300
QY 301 SIGFGVDTWVYPNITDPEYGLAREYIYCLYWSLTLTITIGETPPPVKDEYLFVIFDL 360
DB 301 SIGFGVDTWVYPNITDPEYGLAREYIYCLYWSLTLTITIGETPPPVKDEYLFVIFDL 360
QY 361 IGVLIIFATIVGNVGSMSNNATRAEFQAKIDAVKHVMQFRKYSKOMEAKVIKWFYLT 420
DB 361 IGVLIIFATIVGNVGSMSNNATRAEFQAKIDAVKHVMQFRKYSKOMEAKVIKWFYLT 420
QY 421 NKKTVDEREVLKPLPAKLRAEIAINVHLSLTKKVRIFQDWEAGLLVELVLKLRPQVSPG 480
DB 421 NKKTVDEREVLKPLPAKLRAEIAINVHLSLTKKVRIFQDWEAGLLVELVLKLRPQVSPG 480
QY 481 DYICRKGDIKEMYYIIKEGKLVAVDDGVTQYALLSAGSCFGEISILNKGSKGNRRTA 540
DB 481 DYICRKGDIKEMYYIIKEGKLVAVDDGVTQYALLSAGSCFGEISILNKGSKGNRRTA 540

```

QY 541 NIRSGLYSDFCLSKODLMEAVTEAPDAKKVLEERGRIILMKGLLDENEVAASMEYDVQ 600
 DB 541 NIRSGLYSDFCLSKODLMEAVTEYDPDAKKVLEERGRIILMKGLLDENEVAASMEYDVQ 600
 QY 601 EKLEQLETNMDTLYTRFARLLAEVTAQOQKLKORITVLETKMKQNHEDDYLSDGINTPEP 660
 DB 601 EKLEQLETNMDTLYTRFARLLAEVTAQOQKLKORITVLETKMKQNHEDDYLSDGINTPEP 660
 QY 661 TAAE 664
 DB 661 TAAE 664

RESULT 7
 AAE37219
 ID AAE37219 standard; protein; 664 AA.
 XX
 AC AAE37219;
 XX
 DT 07-AUG-2003 (first entry)
 XX
 DE Rat CNG channel alpha subunit wild-type protein.
 XX
 KW Rat; G protein-coupled receptor; cyclic nucleotide-gated channel; GPCR;
 KW cyclic nucleotide-gated channel; CNG channel.
 XX
 OS Rattus norvegicus.
 XX
 PN WO2003038039-A2.
 XX
 PD 08-MAY-2003.
 XX
 PF 25-OCT-2002; 2002WO-US034122.
 XX
 PR 26-OCT-2001; 2001US-0330663P.
 PR 04-MAR-2002; 2002US-00087217.
 XX
 PA (APTU-) APTUS PHARM INC.
 XX
 PI Yao Y, Cao L;
 XX
 DR WPI; 2003-430510/40.
 DR N-PSDB; AAD56239.
 XX
 PT New host cell comprising first and second nucleic acids with promoters
 PT that encode exogenous G protein-coupled receptor and cyclic nucleotide-
 PT gated channel, respectively, useful for identifying agents that modulate
 PT GPCR activity.
 XX
 PS Claim 13; Page 78-80; 98pp; English.
 XX
 CC The invention relates to compositions and methods for identifying G
 CC protein-coupled receptor (GPCR), ligands and compounds that modulate GPCR
 CC mediated activities. The invention also provides an host cell comprising
 CC first and second nucleic acids with promoters that encode exogenous G
 CC protein-coupled receptor and cyclic nucleotide-gated (CNG) channel
 CC respectively. The host cells are useful for identifying agents that
 CC modulate an activity mediated by a GPCR. The present sequence is rat CNG
 CC channel alpha subunit wild-type protein
 XX
 SQ Sequence 664 AA;

Query Match 99.3%; Score 3449; DB 6; Length 664;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 661; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MMTKSNVKSPPANNHHPPPSIKANGKDDHRAGRPSQVAADDDTSPELQRLAEMDT 60
 DB 1 MMTKSNVKSPPANNHHPPPSIKANGKDDHRAGRPSQVAADDDTSPELQRLAEMDT 60
 QY 61 PRRGGGFORIVRLVGIWIRWANKNFREERPRPDSFLERFRGPBLQVTTWTHQGGDKGKD 120
 DB 61 PRRGGGFORIVRLVGIWIRWANKNFREERPRPDSFLERFRGPBLQVTTWTHQGGDKGKD 120

RESULT 8

AAG79528

ID AAG79528 standard; protein; 664 AA.

XX

AC AAG79528;

XX

DT 03-DEC-2002 (first entry)

XX

DE Mouse HBMYCNG.

XX

KW Human; cation channel; cyclic nucleotide gated; HBMYCNG;
 KW ion channel-related disorder; stroke; depression; liver disease;
 KW Alzheimer's disease; Parkinson's disease; arrhythmia; diabetes;
 KW chronic pain; hypercalcaemia; hypocalcaemia; hypercalciuria; anxiety;
 KW hypocalciuria; gastrointestinal disorder; renal disease.

XX

OS Mus musculus.

XX

PN WO200268471-A2.

XX

PD 06-SEP-2002.

XX

PF 21-DEC-2001; 2001WO-US050413.

XX

PR 21-DEC-2000; 2000US-0257865P.

XX

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX

PI Feder J, Mintier G, Ramanathan C, Westphal R;

XX

DR WPI; 2002-691655/74.

QY 121 GEGKTKKKFELFVLDPAGDWYRWFVVIAMPVLYNWCLLVARACFSDLQRNVFVWLVL 180
 DB 121 GEGKTKKKFELFVLDPAGDWYRWFVVIAMPVLYNWCLLVARACFSDLQRNVFVWLVL 180
 QY 181 DYPSDTVYIADLIIRLTGFLQGLLVKDPKKLRDNYIHTLOPKLDVASIIPTDLIYFAY 240
 DB 181 DYPSDTVYIADLIIRLTGFLQGLLVKDPKKLRDNYIHTLOPKLDVASIIPTDLIYFAY 240
 QY 241 GIHSPEVRNRLHFAFMFEFFDRTRTSYPNIFRISNLVLYIIVIHWNACIYVVISK 300
 DB 241 GIHSPEVRNRLHFAFMFEFFDRTRTSYPNIFRISNLVLYIIVIHWNACIYVVISK 300
 QY 301 SIGFGVDTWVYPNITDPEYGYLAREYIYCLYXWSTLTLTITGETPPPVKDEEYLVIFDFEL 360
 DB 301 SIGFGVDTWVYPNITDPEYGYLAREYIYCLYXWSTLTLTITGETPPPVKDEEYLVIFDFEL 360
 QY 361 IGVLIIPATIVGNVGSIMSNMNAFQAKIDAVKHVMQFRKYSKDMEAKVIKWFYDLWT 420
 DB 361 IGVLIIPATIVGNVGSIMSNMNAFQAKIDAVKHVMQFRKYSKDMEAKVIKWFYDLWT 420
 QY 421 NKKTVDEREVLKMLPAKLAETAINVHLSLTKKVRIFQDWEAGLLVELVLKRPQVSPG 480
 DB 421 NKKTVDEREVLKMLPAKLAETAINVHLSLTKKVRIFQDWEAGLLVELVLKRPQVSPG 480
 QY 481 DYICRKGDIGKEMYIIKEGKLAVVADDGVTQVALLSAGSCFGEISILNKGSKWGNRRTA 540
 DB 481 DYICRKGDIGKEMYIIKEGKLAVVADDGVTQVALLSAGSCFGEISILNKGSKWGNRRTA 540
 QY 541 NIRSGLYSDFCLSKODLMEAVTEAPDAKKVLEERGRIILMKGLLDENEVAASMEYDVQ 600
 DB 541 NIRSGLYSDFCLSKODLMEAVTEYDPDAKKVLEERGRIILMKGLLDENEVAASMEYDVQ 600
 QY 601 EKLEQLETNMDTLYTRFARLLAEVTAQOQKLKORITVLETKMKQNHEDDYLSDGINTPEP 660
 DB 601 EKLEQLETNMDTLYTRFARLLAEVTAQOQKLKORITVLETKMKQNHEDDYLSDGINTPEP 660
 QY 661 TAAE 664
 DB 661 TAAE 664

XX	New human HBMVCMG genes, useful for treating ion channel-related disorders e.g. stroke, anxiety and depression, Alzheimer's or Parkinson's disease, diabetes or arrhythmia.
XX	Disclosure; Fig 4; 177pp; English.
XX	The sequences given in AAG79526-29 represent rabbit, cow, mouse and rat versions of the human cation channel polypeptide designated HBMVCMG.
CC	HBMVCMG is a human cyclic nucleotide gated cation channel with six transmembrane domains. HBMVCMG genes are useful for treating ion channel-related disorders, e.g. stroke, anxiety and depression, Alzheimer's or Parkinson's disease, arrhythmia, diabetes, chronic pain, hypercalcaemia, hypocalcaemia, hypercalciuria, hypocalciuria, gastrointestinal disorders, ion disorders or renal or liver disease
XX	
XX	Sequence 664 AA;
Query Match	97.4%; Score 3384; DB 5; Length 664;
Best Local Similarity	97.6%; Pred. No. 0;
Matches 648; Conservative	3; Mismatches 13; Indels 0; Gaps 0;
QY	1 MMTEKSGVKSSPANNHHPPPSIKANGKDDHRAGSRPQSAADDTSPQLRLAEMDT 60
Db	1 MMTEKSGVKSSPANNHHPPPSIKANGKDDHRAGSRPQSAADDTSSLQLRLAEMDT 60
QY	61 PRRGCGFORIVLGVIRDWANKNFRPEERPDSELERFGRPELOTVTTHOGDDKGKD 120 :
Db	61 PRRGCGFRILRVGLIIRDWANKNFRPEERPDSELERFGRPELOTVTPHGGGKGDKD 120
QY	121 GEKGTKKKKELFYLDPAGDWYYRWLFVIAMPVLVNWCLLVARACFSLQRIYFVVWLVL 180
Db	121 GEKGTKKKKELFYLDPAGDWYYRWLFVIAMFVLVNWCLLVARACFSDLRNYFVVWLVL 180
QY	181 DYSDTVYIADLIIRLTGFLEOGLVKDPKILRDNIHTITQPKLDVASIIPDLIFAV 240
Db	181 DYSDTVYIADLIIRLTGFLEOGLVKDPKKJRDNIHTITQPKLDVASIIPDLIFAV 240
QY	241 GIHSPEVRNRLHFARMFEFDRTETSTYPNIFRISNLVLYIIVIHWNACYIYVTSK 300
Db	241 GIHSPEVRNRLHFARMFEFDRTETSTYPNIFRISNLVLYIIVIHWNACYIYATSK 300
QY	301 SIGFGVDTWYPNITDPEYGVLAREYIYCLYWSTILTITIGETPPPVDDEYLFVFDFL 360
Db	301 SIGFGVDTWYPNITDPEYGVLAREYIYCLYWSTILTITIGETPPPVDDEYLFVFDFL 360
QY	361 IGVLI FATI VGNVGSMI SNMNATRAEFOAKIDAVKHVMQPRKVKDMKAQIKWFYDYLWT 420
Db	361 IGVLI FATI VGNVGSMI SNMNATRAEFOAKIDAVKHVMQPRKVKDMKAQIKWFYDYLWT 420
QY	421 NKKTVDREVVLKNLP AKLRABIAINVHLSTLKVRIFQDWAGLVELVLKRPQVFSFG 480
Db	421 NKKTVDREVVLKNLP AKLRABIAINVHLSTLKVRIFQDCAGLLVELVLKRPQVFSFG 480
QY	481 DYICRKGDIGKEMYII KEGKLAVVADDGVTQYALLSAGSCGETSILNIKSGKMNRRTA 540
Db	481 DYICRKGDIGKEMYII KEGKLAVVADDGVTQYALLSAGSCGETSILNIKSGKMNRRTG 540
QY	541 NIRSIGYSDLFCLSKDDLM EAVTBAPDAKKVLEERGREILMKMGLLDENEVAASMEVDVQ 600
Db	541 TIRSIGYSDLFCLSKDDLM EAVTEYPDAAKVLEERGREILMKEGLLDENEAASMEVDVQ 600
QY	601 EKLEQLETNMOTLYTR FARLLAEYTGAAOKUKORITVILETKMQNHEDDYLDGINTPTPEP 660 :
Db	601 EKLEQLETNMETLYTR FARLLAEYTGAAQQKKQRITVILETKMQNHEDDYLDGINTPTPEP 660
QY	661 TAAE 664
Db	661 AVAE 664
RESULT 9	
AAG79526	

Db 368 IGFGVDTWVYPIITDPEYGYLAREYICLYWSTLTITIGETPPPVKDBEYLFVIFDFLI 427
 QY 362 GVLIFATIVGVNGSMISNNATRAEFQAKIDAVHYMQFRKYSKDMKAEKVIKWFEDYLWLN 421
 Db 428 GVLIFATIVGVNGSMISNNATRAEFQAKIDAVHYMQFRKYSKDMKAEKVIKWFEDYLWLN 487
 QY 422 KKTVDEREVLKPKLPAKRAEIAINVHLSLTKKVRIFQDWEAGLLVELVLKLRPQVFSPGD 481
 Db 488 KKTVDEREVLKPKLPAKRAEIAINVHLSLTKKVRIFQDWEAGLLVELVLKLRPQVFSPGD 547
 QY 482 YICRKGDIKEMWIIKEGKLAHVADGVTQYALLSAGSCFGEISILINIKGSKMGNNRTAN 541
 Db 548 YICRKGDIKEMWIIKEGKLAHVADGVTQYALLSAGSCFGEISILINIKGSKMGNNRTAN 607
 QY 542 IRSLGYSDLFCLSKODLMEAVTEAPDAKKVLEERGREILMKVGLLDENEVAASMEVDVQE 601
 Db 608 IRSLGYSDLFCLSKODLMEAVTEAPDAKKVLEERGREILMKVGLLDENEVAASMEVDVQE 667
 QY 602 KLEQLETNMDTLYTRFARLLAEYTGAKQKQKORITVLETKMKQNHDDYLSGINTPEPT 661
 Db 668 KLEQLETNMDTLYTRFARLLAEYTGAKQKQKORITVLETKMKQNHDDYLSGINTPEPT 727
 QY 662 AAE 664
 Db 728 AAE 730
 RESULT 10
 AAG79527
 ID AAG79527 standard; protein; 663 AA.
 XX
 AC AAG79527;
 DT 09-DEC-2002 (first entry)
 DE Cow HBMYCNG.
 XX Human; cation channel; cyclic nucleotide gated; HBMYCNG;
 KW ion channel-related disorder; stroke; depression; liver disease;
 KW Alzheimer's disease; Parkinson's disease; arrhythmia; diabetes;
 KW chronic pain; hypercalcaemia; hypocalcaemia; hypercalciuria; anxiety;
 KW hypocalciuria; gastrointestinal disorder; renal disease.
 OS Bos taurus.
 XX
 PN WO200268471-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 21-DEC-2001; 2001WO-US050413.
 XX
 PR 21-DEC-2000; 2000US-0257865P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Feder J, Mintier G, Ramanathan C, Westphal R;
 XX WPI; 2002-691655/74.
 DR
 PT New human HBMYCNG genes, useful for treating ion channel-related
 PT disorders e.g. stroke, anxiety and depression, Alzheimer's or Parkinson's
 PT disease, diabetes or arrhythmia.
 XX
 PS Disclosure; Fig 4; 177pp; English.
 XX
 CC The sequences given in AAG79526-29 represent rabbit, cow, mouse and rat
 CC versions of the human cation channel polypeptide designated HBMYCNG.
 CC HBMYCNG is a human cyclic nucleotide gated cation channel with six
 CC transmembrane domains. HBMYCNG genes are useful for treating ion channel-
 CC related disorders, e.g. stroke, anxiety and depression, Alzheimer's or
 CC Parkinson's disease, arrhythmia, diabetes, chronic pain, hypercalcaemia,
 CC hypocalcaemia, hypercalciuria, hypocalciuria, gastrointestinal disorders,
 CC ion disorders or renal or liver disease

XX Sequence 663 AA;
 SQ Query Match 92.2%; Score 3204.5; DB 5; Length 663;
 Best Local Similarity 92.3%; Pred. No. 1.2e-306;
 Matches 610; Conservative 27; Mismatches 23; Indels 1; Gaps 1;
 QY 2 MTEKNGVKSPANNHHPPPSIKANGKDDHRAGSRPQSVAADDTSPELQRLAEMDTP 61
 Db 1 MTEKANGVKSPANNHHPPAIKASGKDDHRASSRPQSAAA-DDTSSELQQLAEMDAP 59
 QY 62 RRGRGGFORIVLGVIRDWANKNFRPEEPDPSFLERPRGPELQTVTTTHQDDDKGKDG 121
 Db 60 QORRGGFRIARLVGLREWYRNFRPEEPDPSFLERPRGPELHTVTITQQDGKDGKDG 119
 QY 122 EGKGTKKKPELVLDPAQDWYRMLFVIAMPVLYNWCILLVARACFSDQRNYFVVMVLVD 181
 Db 120 EGKGTKKKPELVLDPAQDWYRMLFVIAMPVLYNWCILLVARACFSDQKGYIYVMVLVD 179
 QY 182 YFSDTVYIADLIIRLTGTFLEQGLLVKDPKKLRDNYIHTLOFKLDVASIIPDILIYFVAVG 241
 Db 180 YVSDVVIADLIIRLTGTFLEQGLLVKDTKKLRDNYIHTMQPKLDVASIIPDILIYFVAVG 239
 QY 242 IHSPEVFNRLHFAFMFEFFDRTETRTSYNIPRISNLVLYILVIHWNACIYYVVISKS 301
 Db 240 IHNPEVFNRLHFAFMFEFFDRTETRTSYNIPRISNLVLYILVIHWNACIYYVVISKS 299
 QY 302 IGFGVDTWVYPIITDPEYGYLAREYICLYWSTLTITIGETPPPVKDBEYLFVIFDFLI 361
 Db 300 IGFGVDTWVYPIITDPEYGYLSREYIYCLYWSTLTITIGETPPPVKDBEYLFVIFDFLI 359
 QY 362 GVLIFATIVGVNGSMISNNATRAEFQAKIDAVHYMQFRKYSKDMKAEKVIKWFEDYLWLN 421
 Db 360 GVLIFATIVGVNGSMISNNATRAEFQAKIDAVHYMQFRKYSKDMKAEKVIKWFEDYLWLN 419
 QY 422 KKTVDEREVLKPKLPAKRAEIAINVHLSLTKKVRIFQDWEAGLLVELVLKLRPQVFSPGD 481
 Db 420 KKSVDEREVLKPKLPAKRAEIAINVHLSLTKKVRIFQDWEAGLLVELVLKLRPQVFSPGD 479
 QY 482 YICRKGDIKEMWIIKEGKLAHVADGVTQYALLSAGSCFGEISILINIKGSKMGNNRTAN 541
 Db 480 YICRKGDIKEMWIIKEGKLAHVADGVTQYALLSAGSCFGEISILINIKGSKMGNNRTAN 539
 QY 542 IRSLGYSDLFCLSKODLMEAVTEAPDAKKVLEERGREILMKVGLLDENEVAASMEVDVQE 601
 Db 540 IRSLGYSDLFCLSKODLMEAVTEAPDAKKVLEERGREILMKVGLLDENEVAASMEVDVQE 599
 QY 602 KLEQLETNMDTLYTRFARLLAEYTGAKQKQKORITVLETKMKQNHDDYLSGINTPEPT 661
 Db 600 KLEQLETNMDTLYTRFARLLAEYTGAKQKQKORITVLETKMKQNHDDYLSGINTPEPT 659
 QY 662 A 662
 Db 660 A 660
 RESULT 11
 ABG74912
 ID ABG74912 standard; protein; 663 AA.
 XX
 AC ABG74912;
 XX
 DT 10-JUL-2003 (first entry)
 XX
 DE Bovine CNG ion channel alpha3 subunit.
 XX
 KW CNG ion channel; alpha3 subunit; phosphodiesterase; drug screening;
 KW cyclic nucleotide gated ion channel; CAMP sensitivity; adenylyl cyclase;
 KW cyclic adenosine monophosphate; cyclic guanosine monophosphate; bovine;
 KW G protein-coupled receptor; calcium concentration.
 XX
 OS Bos taurus.
 XX

gated (CNG) ion channel which comprises subunits in which the position corresponding to Thr537 of the bovine alpha3 subunit is changed so as to increase sensitivity to cyclic adenosine monophosphate (cAMP) and/or selectivity for cAMP over cyclic guanosine monophosphate, relative to the wild type. The invention also describes a modified bovine CNG ion channel alpha3 subunit in which the position corresponding to Thr537 is substituted by any residue except Ser. The products of the invention are used (i) to measure intracellular cAMP concentrations and (ii) to determine the effect of ligands, agonists and antagonists on G protein-coupled receptors, also of other activators and inhibitors on other proteins that regulate the intracellular cAMP concentration. Cell lines that express the novel channel are used (i) to measure the intracellular calcium concentration, especially for characterisation of pharmaceutical and/or pharmacological substances that modulate intracellular cAMP concentration and (ii) to characterise G protein-coupled receptors, adenylyl cyclase, phosphodiesterases or other proteins that regulate cAMP, particularly for drug screening. The channel is modified at only one position but has the same sensitivity as known double mutants and provides a rapid and simple cellular measuring system that is effective and universally applicable for drug screening and characterisation. This sequence represents the mutant bovine CNG ion channel alpha3 subunit, T537V, described in the disclosure of the invention

XX SQ Sequence 663 AA;

Query Match 92.1%; Score 3199.5; DB 6; Length 663;
Best Local Similarity 92.1%; Pred. No. 3.7e-306;
Matches 609; Conservative 27; Mismatches 24; Indels 1; Gaps 1;

QY 2 MTEKSGVSSPANNHHPPPSIKANGKDDHAGSRPSQVADDDTSPBLQRLAEMDTP 61
Db 1 MTEKANGVSSPANNHHAPPKAGSKDDHRRASSRPSQAAA-DDTSSLOQLAEMDAP 59
QY 62 RRGGRGQRIARLVGVIRWANKNFRPEERPSFLERFRGPELQTVTTHGGDKGKOG 121
Db 60 QQRGGFRRLARLVGVIRWAYNFRPEERPSFLERFRGPELHVTVOGGDKGKOG 119
QY 122 EGGTKKKKFFELVDLPAGDWYRMLFVIAMPVLVNWCLLVARACFSDLQRYVFWVLVD 181
Db 120 EGGTKKKKFFELVDLPAGDWYRMLFLIALPVLYNWCLLVARACFSDLQRYVFWVLVD 179
QY 182 YPSDVTWYIADLIIRLTGFEGLGKLVKPKIDPNVHTHTQKLDVASIIPDILYFVG 241
Db 180 YSDVVTIADLFRLTGTGLEGLLVKDKKLDNDVHTHTMQKLDVASIIPDILYFVG 239
QY 242 IHSPEVRNRLHFAFMFEFFDRTETRTSYPNIFRISNLVLYTHWNACIYVWISKS 301
Db 240 IHNPEVRNRLHFAFMFEFFDRTETRTSYPNIFRISNLVLYTHWNACIYVWISKS 299
QY 302 IGRGVTWYVYVNTDPEYGLAREYIYCLVWSLTTLTIGETPPPVKDEYLVFDFLI 361
Db 300 IGRGVTWYVYVNTDPEYGLAREYIYCLVWSLTTLTIGETPPPVKDEYLVFDFLI 359
QY 362 GVLIIFATVGVGSMISNNMTRAEFOAKIDAVKHYMQPKVSKDMEAKVWKEDYLTWN 421
Db 360 GVLIIFATVGVGSMISNNMTRAEFOAKIDAVKHYMQPKVSKDMEAKVWKEDYLTWN 419
QY 422 KKTVDREVKNLPKALRABIAINVLHSTLTKVRIIFQDMEAGLLVEILVKLRQVPSGD 481
Db 420 KKSVDREVKNLPKALRABIAINVLHSTLTKVRIIFQDCEAGLLVEILVKLRQVPSGD 479
QY 482 YICRKGDIKEMVIIKEGKLAVADGVTOYALLSAGSCFGETSILNIGSKXMGNRRTAN 541
Db 480 YICRKGDIKEMVIIKEGKLAVADGVTOYALLSAGSCFGETSILNIGSKXMGNRRTAN 539
QY 542 IRSIGYSDLPCLSKDLDMEAVTEAPDAKKVLEERGREILMKGLDENVAASMEVDVQ 601
Db 540 IRSIGYSDLPCLSKDLDMEAVTEAPDAKKVLEERGREILMKGLDENVAASMEVDVQ 599
QY 602 KLSQLETNMDTLTRFARLLAEYTGAAQKLKQRTVLETKQKQNHEDDYLSDGINTPEPT 661
Db 600 KLSQLETNMDTLTRFARLLAEYTGAAQKLKQRTVLETKQKQNHEDDYLSDGINTPEPT 659

QY 662 A 662
Db 660 A 660

RESULT 13
ABG74913
ID ABG74913 standard; protein; 663 AA.
AC ABG74913;
XX 10-JUL-2003 (first entry)
XX Bovine CNG ion channel alpha3 subunit mutant T537M.
XX CNG ion channel; alpha3 subunit; phosphodiesterase; drug screening;
XX cyclic nucleotide gated ion channel; cAMP sensitivity; adenylyl cyclase;
XX cyclic adenosine monophosphate; cyclic guanosine monophosphate; bovine;
XX G protein-coupled receptor; calcium concentration; mutant; mutein.
XX Bos taurus.
XX Synthetic.
XX Key Location/Qualifiers
FT Misc-difference 537 /label= T537M
FT FT /note= "Wild type Thr is replaced by Met"
XX WO2003014149-A2.
XX 20-FEB-2003.
XX 06-AUG-2002; 2002WO-EP008756.
XX 08-AUG-2001; 2001DE-01038876.
XX (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
XX Kaupp UB, Seifert R, Gauss R, Koerschen H;
XX WPI; 2003-256538/25.
XX N-PSDB; ABX94805.
XX New genetically modified cyclic nucleotide gated ion channel, useful e.g.
XX for drug screening, has increased sensitivity, or selectivity, for cyclic
XX adenosine monophosphate.
XX Example 1-4; Page 81-84; 93pp; German.
XX This invention describes a novel genetically modified cyclic nucleotide
XX gated (CNG) ion channel which comprises subunits in which the position
XX corresponding to Thr537 of the bovine alpha3 subunit is changed so as to
XX increase sensitivity to cyclic adenosine monophosphate (cAMP) and/or
XX selectivity for cAMP over cyclic guanosine monophosphate, relative to the
XX wild type. The invention also describes a modified bovine CNG ion channel
XX alpha3 subunit in which the position corresponding to Thr537 is
XX substituted by any residue except Ser. The products of the invention are
XX used (i) to measure intracellular cAMP concentrations and (ii) to
XX determine the effect of ligands, agonists and antagonists on G protein-
XX coupled receptors, also of other activators and inhibitors on other
XX proteins that regulate the intracellular cAMP concentration. Cell lines
XX that express the novel channel are used (i) to measure the intracellular
XX calcium concentration, especially for characterisation of pharmaceutical
XX and/or pharmacological substances that modulate intracellular cAMP
XX concentration and (ii) to characterise G protein-coupled receptors,
XX adenylyl cyclase, phosphodiesterases or other proteins that regulate cAMP,
XX particularly for drug screening. The channel is modified at only one
XX position but has the same sensitivity as known double mutants and
XX provides a rapid and simple cellular measuring system that is effective
XX and universally applicable for drug screening and characterisation. This
XX sequence represents the mutant bovine CNG ion channel alpha3 subunit,
XX T537M, described in the disclosure of the invention

QY	Sequence	663 AA;
QY	2 MTEKSNVGSPPANNHHPSPSIKANGKDDHRRAGSRPOSVAADDDTSPFLQRLAEMDTP 61	
Db	1 MTEKANGVSSPPANNHHPAPKAASKGDDHRRASRRPOSAAA-DUTSELQQAENMAP 59	
QY	62 RRGGRGQRIVRLVGVIRDWANKNFREERPRPDSFLERPRGPELQVITTHQGDGKGGKDG 121	
Db	60 QQRGGGFRRIARLVGLREWAVNFREERPRPDSFLERPRGPELHTVITQQGDGKGGKDG 119	
QY	122 EKGTKKKKPELVLDIPAGDWMYRWLFIAMFVLYNWCLLVABACSDIQRNYFVWVLVD 181	
Db	120 EKGTKKKKPELVLDIPAGDWMYRWLFIAMFVLYNWCLLVABACFSDIQRNYFVWVLVD 179	
QY	182 YFSDTVIADLIIRLTGTFLEQGLLVKDKPKLRDNYIHTQKLDVASTIPTDLIYFVAG 241	
Db	180 YUSDVVIADLIIRLTGTFLEQGLLVKDKPKLRDNYIHTQKLDVASTIPTDLIYFVAG 239	
QY	242 IHSPEVRNRLHFARMFPEFFORTETRTSYNPIFRISNLVLVILVIHWNACIYVVISKS 301	
Db	240 IHNPEVRNRLHFARMFPEFFORTETRTSYNPIFRISNLVLVILVIHWNACIYVVISKS 299	
QY	302 IGRGVDTWVYFNITDPEYGLVAREYIYCLYWSLTLLTITGETPPPVKDEEYLVFVDFLI 361	
Db	300 IGRGVDTWVYFNITDPEYGLVAREYIYCLYWSLTLLTITGETPPPVKDEEYLVFVDFLI 359	
QY	362 GVLIFFATIVGNVGSMTSNNATRAEPQAKIDAVKHYMQFRKYSKDMKAKVKEWDYLTWN 421	
Db	360 GVLIFFATIVGNVGSMTSNNATRAEPQAKIDAVKHYMQFRKYSKDMKAKVKEWDYLTWN 419	
QY	422 KKTVDSEVLKVLPAKRAEIAINVLHSLTKKVRIFQDWEAGLLVVLKLPQVFSFGD 481	
Db	420 KKSVDSEVLKVLPAKRAEIAINVLHSLTKKVRIFQDWEAGLLVVLKLPQVFSFGD 479	
QY	482 YICRKGDIKEMYIIEKGLVAVDDGVTVQYALLSAGSCFGEISILINIKSGKMGNRRTAN 541	
Db	480 YICRKGDIKEMYIIEKGLVAVDDGVTVQYALLSAGSCFGEISILINIKSGKMGNRMAN 539	
QY	542 IRLSGVSDILFCISKDLMFAVTEADPAKKVLSRGERILMKGLLDENEVAASVEVDVQE 601	
Db	540 IRLSGVSDILFCISKDLMFAVTEADPAKKVLSRGERILMKGLLDENEVAASVEVDVQE 599	
QY	602 KLEQLETNMDTLTYTRFARLLAEYTGAAQKLQRITVLETKMKONHEDDYLSDGINTPEPT 661	
Db	600 KLEQLETNMDTLTYTRFARLLAEYTGAAQKLQRITVLETKMKONHEDDYLSDGINTPEPT 659	
QY	662 A 662	
Db	660 A 660	
RESULT 14		
AAE04894		
ID	AAE04894 standard; protein; 664 AA.	
AC	AAE04894;	
CC		
DT	10-SEP-2001 (first entry)	
DE	Human transporter and ion channel-7 (TRICH-7) protein.	
KW	Human; transporter and ion channel-7; TRICH-7; vaccine; cystic fibrosis; gene therapy; amphotrophic lateral sclerosis; amnesia; muscular dystrophy; hypertension; angina; neurological disorder; asthma; bipolar disorder; dementia; depression; Alzheimer's disease; epilepsy; mood; arrhythmia; Pick's disease; ischaemic cerebrovascular disease; AIDS; anxiety; stroke; Huntington's disease; Parkinson's disease; cerebral neoplasm; allergy; demyelinating disease; mental disorder; Schizophrenia; polynomyositis; muscle disorder; cardiomyopathy; cataract; myocardiitis; Grave's disease;	

Search completed: May 12, 2004, 11:13:44
Job time : 62 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 12, 2004, 11:12:35 ; Search time 23 seconds
(without alignments)
1490.419 Million cell updates/sec

Title: US-10-087-217A-8
Perfect score: 3475
Sequence: 1 MMTEKSGVKSFPANNHH.....NHEDDYLSDGINTPEPTAAE 664

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2.6/prodata/2/iaa/5A_COMB.pep.*
2: /cgn2.6/prodata/2/iaa/5B_COMB.pep.*
3: /cgn2.6/prodata/2/iaa/6A_COMB.pep.*
4: /cgn2.6/prodata/2/iaa/6B_COMB.pep.*
5: /cgn2.6/prodata/2/iaa/6CTUS_COMB.pep.*
6: /cgn2.6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2030	58.4	690	4	US-09-275-252A-19
2	1323	38.1	261	4	US-09-275-252A-18
3	634	18.2	129	4	US-08-997-685A-46
4	584	16.8	170	4	US-09-358-383C-27
5	573.5	16.5	126	4	US-08-997-685A-58
6	532.5	15.3	319	4	US-09-358-383C-22
7	526.5	15.2	126	4	US-08-997-685A-57
8	523.5	15.1	910	4	US-08-997-685A-2
9	513	14.8	749	4	US-08-997-685A-10
10	486.5	14.0	528	4	US-08-997-685A-4
11	474	13.6	537	4	US-08-997-685A-12
12	448	12.9	506	4	US-08-997-685A-6
13	446	12.8	988	4	US-09-614-480-2
14	446	12.8	988	4	US-10-162-012-5
15	440	12.7	988	4	US-10-162-012-12
16	424.5	12.2	962	4	US-09-614-480-9
17	424.5	12.2	962	4	US-09-694-777A-3
18	423.5	12.2	962	4	US-09-694-777A-24
19	423	12.2	960	4	US-09-694-777A-21
20	417	12.0	989	4	US-09-694-777A-4
21	416	12.0	989	4	US-09-694-777A-23
22	415.5	12.0	987	4	US-09-694-777A-22
23	413	11.9	1102	4	US-09-358-383C-36
24	407.5	11.7	1284	4	US-09-343-494-9
25	407.5	11.7	1284	4	US-08-358-383C-11
26	401	11.5	1107	4	US-09-358-383C-16
27	394	11.3	1159	2	US-08-956-242-13

28	394	11.3	1159	3	US-09-351-215-13	Sequence 13, Appl
29	394	11.3	1159	3	US-09-226-012-2	Sequence 2, Appl
30	394	11.3	1159	3	US-09-226-012-4	Sequence 4, Appl
31	394	11.3	1159	4	US-09-358-383C-10	Sequence 10, Appl
32	394	11.3	1159	4	US-09-275-252A-12	Sequence 12, Appl
33	390.5	11.2	888	2	US-08-956-242-4	Sequence 4, Appl
34	390.5	11.2	888	3	US-09-351-215-4	Sequence 4, Appl
35	385.5	11.1	1017	4	US-09-600-776-6	Sequence 6, Appl
36	381.5	11.0	1083	4	US-09-600-776-2	Sequence 2, Appl
37	381.5	11.0	1083	4	US-09-343-494-1	Sequence 1, Appl
38	381	11.0	189	4	US-09-358-383C-25	Sequence 25, Appl
39	380	10.9	1083	4	US-09-358-383C-2	Sequence 2, Appl
40	378.5	10.9	1082	4	US-09-336-643A-20	Sequence 20, Appl
41	319.5	9.2	857	4	US-09-275-252A-11	Sequence 11, Appl
42	300	8.6	57	4	US-09-275-252A-38	Sequence 38, Appl
43	286.5	8.2	597	4	US-09-275-252A-7	Sequence 7, Appl
44	265	7.6	57	4	US-09-275-252A-39	Sequence 39, Appl
45	254	7.3	542	4	US-09-358-383C-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-09-275-252A-19
; Sequence 19, Application US/09275252A
; Patent No. 6641997
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/09/275,252A
; CURRENT FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-275-252A-19

Query Match 58.4%; Score 2030; DB 4; Length 690;
Best Local Similarity 61.7%; Pred. No. 9.9e-193;
Matches 407; Conservative 84; Mismatches 131; Indels 38; Gaps 7;

QY	23	PSIKANGDDHRRAGSRPQSVAAADDTSPLOQLAEMDTPRRGGF-----QRI 71
DB	25	PDIE---KEIRRMENGACSFSEDDSDSAVTSSENEP-HARGSFYSKLRKGGSQRE 80
QY	72	VRLVGVR-----DWANKPREPEPRDPSFLERPRGPELOTVVTHQDDKG 117
DB	81	QYLPGAIAIFNVNNSNKDQEPPEKKKKKKKKSDKKENKNDPEKK-----KKKKCKE 136
QY	118	GKDGEGKPKK---KFELFLVDPAQDWYRWLFVIAPELVYNWCLLVARACFSDIQRNY 173
DB	137	KKKKEKSKDKKHHKKEVVVDPSGNTYNNWLFCTLPVWNWTVVIARACFELOQSY 196
QY	174	FVWVLVLYFSDTVVIADLIIRLTGFLQGLLVKDPKKLRDNYHTLQKLDVASIIFT 233
DB	197	LEWVILDYVSDIVVYLDIMFVTRTGYLQGLLVKKEELKINKYKSNLQFKLDVLSIPT 256
QY	234	DLIYFVANGHSPEVFPNRLHFAPEFDRTRTTSYNIFRISNLVYILVIHWNAC 293
DB	257	DLLYFKLGNWYPEIRLNRLRFSRMFEFFQRTETRTNYNIFRISNLVYIIVIIHWNAC 316

QY 294 IYVVISKISIGFVDTWYVPIITDPEYGLAREYICLYWSTLTTLTTIGETPPPVKDBEYL 353
Db 317 VFTSISKAIGFNDTWYVPIITDPEYGLAREYICLYWSTLTTLTTIGETPPPVKDBEYL 376
QY 354 FVIFDFLIGVLIFATIVGVNISMNNATRAEFQAKIDAVKHVMQPRKYSKDMKAEKVIK 413
Db 377 FVVVDFLIGVLIFATIVGVNISMNNATRAEFQAKIDAVKHVMQPRKYSKDMKAEKVIK 436
QY 414 WFDYLTWTKTVDREVLKMLPAKLRABIAINHLSTLTKVRIPQDWEAGLLVELVLKLR 473
Db 437 WFDYLTWTKTVDREVLKMLPAKLRABIAINHLSTLTKVRIPQDWEAGLLVELVLKLR 496
QY 474 PQVPSPDYICRKGDIKGMWIIKEGKLVAVDDGVTOYALLSAGSCFGEISILINIKGSK 533
Db 497 PQVPSPDYICRKGDIKGMWIIKEGKLVAVDDGVTOYALLSAGSCFGEISILINIKGSK 556
QY 534 MGNRTANIRSLGSDYDLFCLSKDLMBAVTEAPDAKKVLEERGRIILMKGMLLDENEV-A 592
Db 557 AGNRRTANIKSIGSDYDLFCLSKDLMBAVTEAPDAKKVLEERGRIILMKGMLLDENEV-A 616
QY 593 ASMEVDVQEKLEQLETNMDITLTFARLLAETGAQOKLQRTVLTETKMKQNHEDDYL 652
Db 617 GSDPKDLEKXVTRMEGSDYDLFCLSKDLMBAVTEAPDAKKVLEERGRIILMKGMLLDENEV-A 676

RESULT 2
US-09-275-252A-18
; Sequence 18, Application US/09275252A
; Patent No. 6641997
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/09/275,252A
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-275-252A-18

Query Match 38.1%; Score 1323; DB 4; Length 261;
Best Local Similarity 97.7%; Pred. No. 4.3e-123;
Matches 255; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 294 IYVVISKISIGFVDTWYVPIITDPEYGLAREYICLYWSTLTTLTTIGETPPPVKDBEYL 353
Db 1 IYVVISKISIGFVDTWYVPIITDPEYGLAREYICLYWSTLTTLTTIGETPPPVKDBEYL 60
QY 354 FVIFDFLIGVLIFATIVGVNISMNNATRAEFQAKIDAVKHVMQPRKYSKDMKAEKVIK 413
Db 61 FVIFDFLIGVLIFATIVGVNISMNNATRAEFQAKIDAVKHVMQPRKYSKDMKAEKVIK 120
QY 414 WFDYLTWTKTVDREVLKMLPAKLRABIAINHLSTLTKVRIPQDWEAGLLVELVLKLR 473
Db 121 WFDYLTWTKTVDREVLKMLPAKLRABIAINHLSTLTKVRIPQDWEAGLLVELVLKLR 180
QY 474 PQVPSPDYICRKGDIKGMWIIKEGKLVAVDDGVTOYALLSAGSCFGEISILINIKGSK 533
Db 181 PQVPSPDYICRKGDIKGMWIIKEGKLVAVDDGVTOYALLSAGSCFGEISILINIKGSK 240

QY 534 MGNRTANIRSLGSDYDLFCLSKDLMBAVTEAPDAKKVLEERGRIILMKGMLLDENEV-A 592
Db 241 MGNRTANIRSLGSDYDLFCLSKDLMBAVTEAPDAKKVLEERGRIILMKGMLLDENEV-A 616
RESULT 3
US-08-997-685A-46
; Sequence 46, Application US/08997685A
; Patent No. 6551821
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Kandel, Eric
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
; FILE REFERENCE: 0575/54806
; CURRENT APPLICATION NUMBER: US/08/997,685A
; CURRENT FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 129
; TYPE: PRT
; ORGANISM: rat;
; FEATURE:
; NAME/KEY: NON CONS
; LOCATION: (48)..(49)
; OTHER INFORMATION: gap in alignment
; FEATURE:
; NAME/KEY: NON CONS
; LOCATION: (121)..(122)
; OTHER INFORMATION: gap in alignment
; FEATURE:
; NAME/KEY: NON CONS
; LOCATION: (125)..(126)
; OTHER INFORMATION: gap in alignment
US-08-997-685A-46

Query Match 18.2%; Score 634; DB 4; Length 129;
Best Local Similarity 98.4%; Pred. No. 4.6e-55;
Matches 127; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 464 LLVELVLKLRPQVSPDYICRKGDIKGMWIIKEGKLVAVDDGVTOYALLSAGSCFGE 523
Db 1 LLVELVLKLRPQVSPDYICRKGDIKGMWIIKEGKLVAVDDGVTOYALLSAGSCFGE 60
QY 524 ISILINIKSGMGNRTANIRSLGSDYDLFCLSKDLMBAVTEAPDAKKVLEERGRIILMKG 583
Db 61 ISILINIKSGMGNRTANIRSLGSDYDLFCLSKDLMBAVTEAPDAKKVLEERGRIILMKG 120
QY 584 GLLDENEVA 592
Db 121 GLLDENEVA 129

RESULT 4
US-09-358-383C-27
; Sequence 27, Application US/09358383C
; Patent No. 6518398
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-055CP
; CURRENT APPLICATION NUMBER: US/09/358,383C
; CURRENT FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: USSN 09/119,855
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: domain

Best Local Similarity 82.5%; Pred. No. 2.2e-44;
 Matches 104; Conservative 14; Mismatches 7; Indels 1; Gaps 1;
 QY 462 AGLLVELVLRQVSPGYICRKGDIKEMVILKEGKLAVVADGVQYALLSAGSCF 521
 Db 1 AGLLVELVLRQVYS-GDYICRKGDIKEMVILKEGKLAVVADGVQYALLSAGSYF 59
 QY 522 GEISILNKGKGNRTNIRSGYSDLCFLSKDLMLEAVTEAPDAKKVLEERGRIILM 581
 Db 60 GEISILNKGKGNRTNIRSGYSDLCFLSKDLMLEAVTEAPDAKKVLEERGRIILM 119
 QY 582 KMGLLD 587
 Db 120 KQGLLD 125
 RESULT 8
 US-08-997-685A-2
 ; Sequence 2, Application US/08997685A
 ; Patent No. 6551821
 ; GENERAL INFORMATION:
 ; APPLICANT: The Trustees of Columbia University
 ; APPLICANT: Kandel, Eric
 ; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
 ; FILE REFERENCE: 0575/54806
 ; CURRENT APPLICATION NUMBER: US/08/997,685A
 ; CURRENT FILING DATE: 1997-12-12
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 910
 ; TYPE: PRT
 ; ORGANISM: mouse
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (130)..(148)
 ; OTHER INFORMATION: S1
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (164)..(185)
 ; OTHER INFORMATION: S2
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (208)..(229)
 ; OTHER INFORMATION: S3
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (243)..(271)
 ; OTHER INFORMATION: S4
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (291)..(313)
 ; OTHER INFORMATION: S5
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (332)..(358)
 ; OTHER INFORMATION: P
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (367)..(387)
 ; OTHER INFORMATION: S6
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (472)..(602)
 ; OTHER INFORMATION: CNB
 ; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: AAC53518
 ; DATABASE ENTRY DATE: 1997-12-27
 ; RELEVANT RESIDUES: (1)..(910)
 US-08-997-685A-2

Query March 15.1%; Score 523.5; DB 4; Length 910;
 Best Local Similarity 24.7%; Pred. No. 1.1e-42;

Matches 180; Conservative 137; Mismatches 287; Indels 125; Gaps 28;
 QY 8 GYKSSPANH---NHPPPSIKANG--KDDHRAGSRPOSVAADDTSPEL-----52
 Db 4 GYKPSASNRDSDGNSVFPSPKAPATGPVAADKRLGTPRGAAGKSGHSGVCFKVDGGGG 63
 QY 53 ---QRLAEMDTPRRGRGQRIVLVGVIRWANKNFREERPRPDSFLERFGPELQTV 108
 Db 64 EEPAGSFEDABGRROYGFMQR--QFTSMLOQGVNR-----FSLRMFGSQ---106
 QY 109 TTHQGDGKDGKDGKTKKFE-----LFVLDPAGDMYVWFLVFIAMPVLYNWCLLVA 162
 Db 107 -----KAVEKEQERVKTAGFWIIHPYSDFRFYWDLLMLIMVGNLIPV 151
 QY 163 RACFSDLQRNYFVWLVLDYFSDTVIADLIIRLRGFL--EQGLLVKDPKLRDNYIHT 220
 Db 152 GITFFTEQTT--TPWIIFNVASDTVFLDLIMFNRTGTYNEDSSEIILDPKVIKMYLKS 209
 QY 221 LQFKLDVASIIPDLYFAV--GIHSPE-----VRFN-----RLHFAFMFEFFD 263
 Db 210 -WFVDFISIPVDYIFLIVEKGMSEVYKTARALRIVRFTKILSLRLRLRLRYIYH 268
 QY 264 RTE-----TRTSYPNIFRISNLVLYIIVHMACIYVVISKIGFVDTWVYVN-ITDP 317
 Db 269 QWBEIEFHTVYDLASAVVRIFNLIGMMLLLCHWDGCLQFLVPLLODFPDCWVSLNEMVND 328
 QY 318 EYGYLAREYIYCLYWSLTITLTIG-ETPPPVKDEEYLVIFDFLIGVLIFATIVGVGSM 376
 Db 329 SWG---KOYSYALFKAMSHMLCIGYGAQAPVNSDLIWTLSMIVGATCYAFVFGHATAL 385
 QY 377 ISNMNATRAEFQAKIDAVKHVCFKVKSKDMEAKVTKWFDYLTWNTKKTVDREVLKNLPA 436
 Db 386 IQSLDSRRQYQEKYQVQYMSFHKLPADMRQKHDHYEHRYQG-KIFDEENILSELND 444
 QY 437 KLAETAINVHLSTL-KKVRIIQDWEAGLIVELVLRQVSPGYICRKGDIKEMVIL 495
 Db 445 PLREEI-VNFCRKLVAIPLFANADPNFTAMLKLRFEVQPGDYIIFREGAVGKKMYF 503
 QY 496 IKEGLAVVADGVQYALLSAGSCGEISILNKGKGMNRTNIRSGYSDLCFLSK 555
 Db 504 IQHGVAQVITKS--SKEMKLTGSGYFEGICLLT-KG-----RRTASVRADTYCRLYSLSV 555
 QY 556 DDLMEAVTEAPDAKKVLEERGRIILMKG-----LL-----DENEVAASME 596
 Db 556 DNEVEVLEEYPMRRAFEIVADRLDRIGKKNISILLQKQKDLNTGVFNQENELKQI- 614
 QY 597 VDQEKLEOLETNMDLYTRFARL--LAEYTGAAQKLKORITVLETMKONHEDDYL-SD 653
 Db 615 --VKHDEMVAQIAPPINYPQMTALNCTSSTTPTSRMRTQSPVYATATSLSHSNLHSPSP 672
 QY 654 GINTPEPTA 662
 Db 673 STQTPQPSA 681
 RESULT 9
 US-08-997-685A-10
 ; Sequence 10, Application US/08997685A
 ; Patent No. 6551821
 ; GENERAL INFORMATION:
 ; APPLICANT: The Trustees of Columbia University
 ; APPLICANT: Kandel, Eric
 ; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
 ; FILE REFERENCE: 0575/54806
 ; CURRENT APPLICATION NUMBER: US/08/997,685A
 ; CURRENT FILING DATE: 1997-12-12
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 10
 ; LENGTH: 749
 ; TYPE: PRT
 ; ORGANISM: human
 ; PUBLICATION INFORMATION:


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/ PRIOR APPLICATION NUMBER: US 09/875,423
/ PRIOR FILING DATE: 2001-06-05
/ PRIOR APPLICATION NUMBER: PCT/US01/18398
/ PRIOR FILING DATE: 2001-06-05
/ PRIOR APPLICATION NUMBER: US 60/209,238
/ PRIOR FILING DATE: 2000-06-05
/ PRIOR APPLICATION NUMBER: US 09/875,363
/ PRIOR FILING DATE: 2001-06-05
/ PRIOR APPLICATION NUMBER: PCT/US01/18247
/ PRIOR FILING DATE: 2001-06-05
/ PRIOR APPLICATION NUMBER: US 60/227,068
/ PRIOR FILING DATE: 2000-08-22
/ PRIOR APPLICATION NUMBER: US 09/928,530
/ PRIOR FILING DATE: 2001-08-13
/ PRIOR APPLICATION NUMBER: PCT/US01/25475
/ PRIOR FILING DATE: 2001-08-15
/ PRIOR APPLICATION NUMBER: US 60/226,770
/ PRIOR FILING DATE: 2000-08-21
/ PRIOR APPLICATION NUMBER: US 09/934,421
/ PRIOR FILING DATE: 2001-08-21
/ PRIOR APPLICATION NUMBER: PCT/US01/26096
/ PRIOR FILING DATE: 2001-08-21
/ PRIOR APPLICATION NUMBER: US 60/279,281
/ PRIOR FILING DATE: 2001-03-28
/ PRIOR APPLICATION NUMBER: US 10/109,029
/ PRIOR FILING DATE: 2002-03-28
/ PRIOR APPLICATION NUMBER: PCT/US02/09728
/ PRIOR FILING DATE: 2002-03-28
/ PRIOR APPLICATION NUMBER: US 60/290,288
/ PRIOR FILING DATE: 2001-05-11
/ PRIOR APPLICATION NUMBER: US (not assigned)
/ NUMBER OF SEQ ID NOS: 48
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12
/ LENGTH: 988
/ TYPE: PRT
/ ORGANISM: Rattus norvegicus
/ US-10-162-012-12
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Query Match      12.7%; Score 440; DB 4; Length 988;
Best Local Similarity 25.0%; Pred. No. 2.6e-34;
Matches 149; Conservative 104; Mismatches 219; Indels 124; Gaps 21;

QY 145 WLFVIAMFVLVNWCLVARACFSDLRQNFVWLVLDYFSDTVYIADLIIRLTGFL-EQ 203
Db 217 WDWVILILFTYAIMVYVNVSVFKTKQNN--IAMLVLDSDVDFVLDVILNPHHTFVGP 274
QY 204 GLLVKDPKLRDNYIHTLOPKLDVAGLIIPDLI-----YFVAVGIHS--PEVRFNRLHFAR 257
Db 275 GEVISDPKLRIMNYLKT-MFVIDLLSCLPYDIINAFENVDEGSISSFSLKVVVRLRLGR 333
QY 258 MBEFFDRTRTSYPNIFRISNLVLIV-----IIHWNACIYVVISKSGI----- 303
Db 334 VARKLD-----HYLEVGAADVLLVCVGLVAHVLACIWIY-----SIGDYEVIDEVT 380
QY 304 --FGVDTWTPV---NTDPPYGLARE-----YIYCLYWSLTLTITIG-ETPP 345
Db 381 NTIQDSWLYQLALSIRTP-RYRNTSAGIWEGGSPKDSLYVSSLYFTMTSLTITIGFNTA 439
QY 346 PVKDEEYLFVIFDFLIGLIFATVGNVSGMISNMNATRAEFQAKIDAVKHVMQFRKYSK 405
Db 440 PTTDVEKXFXVAMMMVGSLLYATIFGNVTTFIQOMANTNRYHEMLNNVDFLKLVCVPK 499
QY 406 DMEAKVKNFDYLTWTKTKTVDEREVLKNLPKLAKEIAINVHLSLTKKVRIFQDWEAGLL 465
Db 500 GLSERVMDYIVSTWMSKSGIDTEKVLSCPKDMREADICVHLNRKVFNEHFAFLASDGCL 559
QY 466 VELVLKLRPQVSPGDIYCKRGDIKEMYYIKGKLAIVADDGVTQYALLSAGSCFGEIS 525
Db 560 RALAVEFQTHCAPGDLIYHAGESVDALCFWVSGSLEVIQDEEVV--AILKGDIYFGDIF 617
QY 526 ILNKGSKVGNRRRTAIRSLGYSDFLCLSKDLDMEAV----- 562
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Search completed: May 12, 2004, 11:16:21
Job time : 25 secs

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Db 618 ----WKETTLAH-ACANVRALTYCDLHIIKBEALLKVLDFYAFANSFSRNLITCNLRKR 673
QY 563 ----TEAPDAKKVLEBERGRILMKMGLLDENEVAASMEVD-----VOEKLEQL----- 606
Db 674 IIFRKISDYKKEEERLRQ-----KNEVTLSPVDHPVRKLFQKFKQOKELRNOGS 724
QY 607 -----ETNMDTLYTRFARLLABVTGAQOKLKORITVLETK-----MKQNHED 648
Db 725 AQSDPERSQLQVESRPLQNGASITGTSVVTSQITPIQISLAYVKTSETLKQNRD 780
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 12, 2004, 11:07:49 ; Search time 17 Seconds
(without alignments)
2033.799 Million cell updates/sec

Title: US-10-087-217A-8

Perfect score: 3475

Sequence: 1 MMTEKNGVKSPANNHH.....NHEDYLSGINTPEPTAAE 664

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	3449	99.3	664	1 CNG2 RAT	Q00195 rattus norv
2	3384	97.4	664	1 CNG2 MOUSE	Q82398 mus musculu
3	3231.5	93.0	664	1 CNG2 RABIT	Q28718 oryctolagus
4	3204.5	92.2	663	1 CNG2 BOVIN	Q03041 bos taurus
5	2219.5	63.9	735	1 CNG1 CHICK	Q90805 gallus gall
6	2151.5	61.9	631	1 CNG3 MOUSE	Q9jj28 mus musculu
7	2140	61.6	706	1 CNG3 BOVIN	Q29441 bos taurus
8	2139	61.6	694	1 CNG3 HUMAN	Q16281 homo sapien
9	2131	61.3	682	1 CNG1 ICTPU	P55934 ictalurus p
10	2067	59.5	645	1 CNG3 CHICK	Q90980 gallus gall
11	2044	58.8	690	1 CNG1 BOVIN	Q00194 b cgmpr-gate
12	2034	58.5	686	1 CNG1 HUMAN	P29973 h cgmpr-gate
13	2026	58.3	683	1 CNG1 RAT	Q62927 r cgmpr-gate
14	2017.5	58.1	691	1 CNG1 CANFA	P29974 m cgmpr-gate
15	2012.5	57.9	684	1 CNG1 MOUSE	Q28279 c cgmpr-gate
16	1518	43.7	575	1 CNGX RAT	Q84359 rattus norv
17	1494	43.0	665	1 CNG DROME	Q24278 drosophila
18	1338.5	38.5	733	1 CNG CAEEL	Q03611 caenorhabdi
19	1323	38.1	261	1 CNG2 HUMAN	Q16280 homo sapien
20	778	22.4	909	1 CNG4 HUMAN	Q14028 homo sapien
21	770	22.2	1394	1 CNG4 BOVIN	Q28181 bos taurus
22	524	15.1	910	1 HCN1 RAT	Q9jkb0 rattus norv
23	522.5	15.0	910	1 HCN1 MOUSE	Q88704 mus musculu
24	522	15.0	834	1 HCN2 RAT	Q9jka9 rattus norv
25	522	15.0	863	1 HCN2 MOUSE	Q88703 mus musculu
26	520.5	15.0	822	1 HCN1 RABIT	Q9mzel oryctolagus
27	518	14.9	890	1 HCN1 HUMAN	Q60741 homo sapien
28	484.5	14.2	1203	1 HCN4 HUMAN	Q9y3q4 homo sapien
29	492	14.2	1198	1 HCN4 RAT	Q9jka7 rattus norv
30	490.5	14.1	1175	1 HCN4 RABIT	Q9tv66 oryctolagus
31	490	14.1	889	1 HCN2 HUMAN	Q9ul51 homo sapien
32	481.5	13.9	780	1 HCN3 RAT	Q9jka8 rattus norv
33	479	13.8	774	1 HCN3 HUMAN	Q9p1z3 homo sapien

RESULT 1
CNG2 RAT
ID CNG2 RAT STANDARD; PRT; 664 AA.
AC Q00195;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cyclic-nucleotide-gated olfactory channel (Cyclic-nucleotide-gated
DE cation channel 2) (CNG channel 2) (CNG2) (CNG-2) (OCNCL1).
GN CNGA2 OR CNCG2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Olfactory sensory neuron;
RX MEDLINE=90370115; PubMed=1697649;
RA Dhallan R.S., Yau K.-W., Schrader K.A., Reed R.R.;
RT "Primary structure and functional expression of a cyclic nucleotide-
RT activated channel from olfactory neurons.";
RL Nature 347:184-187(1990).
CC -!- FUNCTION: Odorant signal transduction is probably mediated by a G-
CC protein coupled cascade using cAMP as second messenger. The
CC olfactory channel can be shown to be activated by cyclic
CC nucleotides which leads to a depolarization of olfactory sensory
CC neurons.
CC -!- SUBUNIT: Heterooligomer of OCNCL1 and CNCG2 subunits.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Olfactory neurons.
CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
CC (TC 1.A.1.5) family.
CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
CC -!- CAUTION: It is uncertain whether Met-1 or Met-2 is the initiator.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X55519; CAA39135.1; -;
CC PIR; S11517; S11517.
CC InterPro; IPR000595; cNMP binding.
CC InterPro; IPR005821; Ion Trans.
CC InterPro; IPR001622; K+channel_pore.
CC Pfam; PF000027; cNMP_binding; 1.
CC Pfam; PF00520; Ion trans; 1.
CC SMART; SMC0100; cNMP; 1.
CC PROSITE; PS00888; CNMP_BINDING_1; 1.
CC PROSITE; PS00889; CNMP_BINDING_2; 1.
CC PROSITE; PS00442; CNMP_BINDING_3; 1.
CC Ionic channel; Ion transport; cAMP-binding; Transmembrane;
CC Multigene family; Olfaction.
KW

O88705 mus musculu
O70507 mus musculu
Q8ncm2 homo sapien
Q9ep15 rattus norv
Q83472 rattus norv
O54853 rattus norv
O54852 rattus norv
Q9er47 mus musculu
Q95259 homo sapien
Q50603 mus musculu
O18965 bos taurus
Q9h252 homo sapien

ALIGNMENTS

```

FT DOMAIN 1 142 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 143 162 H1 (POTENTIAL).
FT DOMAIN 163 175 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 176 194 H2 (POTENTIAL).
FT DOMAIN 195 218 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 219 238 H3 (POTENTIAL).
FT DOMAIN 239 276 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 277 299 H4 (POTENTIAL).
FT DOMAIN 300 351 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 352 371 H5 (POTENTIAL).
FT DOMAIN 372 455 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 456 476 H6 (POTENTIAL).
FT DOMAIN 477 664 CYTOPLASMIC (POTENTIAL).
FT NP_BIND 464 586 CAMP (BY SIMILARITY).
FT BINDING 523 538 CAMP (POTENTIAL).
FT BINDING 538 538 CAMP (POTENTIAL).
FT CARBOHYD 381 381 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 212 212 K -> R.
SQ SEQUENCE 664 AA; 76176 MW; 720806950EC27F3C CRC64;

Query Match
Best Local Similarity 99.3%; Score 3449; DB 1; Length 664;
Matches 661; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MMTKSGVKSPPANNHHPPPSIKANGKDDHAGSRPOSVAADDTSPBLQSLAEMDT 60
Db 1 MMTKSGVKSPPANNHHPPPSIKANGKDDHAGSRPOSVAADDTSPBLQSLAEMDT 60

Qy 61 PRRGGGFORIVLVGVIRWANKNFRERPEPSELERGPELQVTTTHOGDDKGGK 120
Db 61 PRRGGGFORIVLVGVIRWANKNFRERPEPSELERGPELQVTTTHOGDDKGGK 120

Qy 121 GEGKGTKKKPELVLDPAAGDWYRWLFVIAFVLYNWCLLVARCFSDLQRYNFWWLVL 180
Db 121 GEGKGTKKKPELVLDPAAGDWYRWLFVIAFVLYNWCLLVARCFSDLQRYNFWWLVL 180

Qy 181 DYFSDTVIADLIIRLTGTFLEOGLLVKDPKKLRDNIHTLOFKLDVASIPTDLYFVAV 240
Db 181 DYFSDTVIADLIIRLTGTFLEOGLLVKDPKKLRDNIHTLOFKLDVASIPTDLYFVAV 240

Qy 241 GIHSPVFRNLLHFARMEFFDRTETRTSPNIFRISNLVLYLVIHWNACIYYVISK 300
Db 241 GIHSPVFRNLLHFARMEFFDRTETRTSPNIFRISNLVLYLVIHWNACIYYVISK 300

Qy 301 SIGFGVDTWVYVNTDPEYGYLAREYIYCLYWSLTLLTIGETPPPVKDEEYLFVDFEL 360
Db 301 SIGFGVDTWVYVNTDPEYGYLAREYIYCLYWSLTLLTIGETPPPVKDEEYLFVDFEL 360

Qy 361 IGVLIPTIYGVNCSMI SNMNATRAEFOAKIDAVKHYMQFRKSKDMEAKVWFYDLWT 420
Db 361 IGVLIPTIYGVNCSMI SNMNATRAEFOAKIDAVKHYMQFRKSKDMEAKVWFYDLWT 420

Qy 421 NKKTVDREVLKNLPKALRABIAINVLHSLTKKVRITFDWEAGLLVELVLRQVPSFG 480
Db 421 NKKTVDREVLKNLPKALRABIAINVLHSLTKKVRITFDWEAGLLVELVLRQVPSFG 480

Qy 481 DYICRKGIDGEMVIIKEGKLAVVADGVTOYALLSAGSCFGEISILNIGSKMGNRRTA 540
Db 481 DYICRKGIDGEMVIIKEGKLAVVADGVTOYALLSAGSCFGEISILNIGSKMGNRRTA 540

Qy 541 NIRSIGVSDLCFLSKDDIMEAVTEAPDAKKVLEERGREILMKGLDENEVAASMEVDVQ 600
Db 541 NIRSIGVSDLCFLSKDDIMEAVTEAPDAKKVLEERGREILMKGLDENEVAASMEVDVQ 600

Qy 601 EKLQLENTMDTLTRFARLLAETGAQOKLQRTIVLETQMKQNHEDDYLSDGINTPEP 660
Db 601 EKLQLENTMDTLTRFARLLAETGAQOKLQRTIVLETQMKQNHEDDYLSDGINTPEP 660

Qy 661 TAEE 664
Db 661 TAEE 664

```

RESULT 2

CNG2_MOUSE STANDARD; PRT; 664 AA.

AC Q82396;

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Cyclic-nucleotide-gated olfactory channel (Cyclic-nucleotide-gated olfactory channel 2) (CNG channel 2) (CNG-2) (CNG2).

DE CNG2 OR CNG2 OR CNG4.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Heart;

RX MEDLINE=96439619; PubMed=8841933;

RA Ruiz M.L., London B., Nadal-Ginard B.;

RT "Cloning and characterization of an olfactory cyclic nucleotide-gated channel expressed in mouse heart.";

RL J. Mol. Cell. Cardiol. 28:1453-1461(1996).

CC -!- FUNCTION: Odorant signal transduction is probably mediated by a G-protein coupled cascade using cAMP as second messenger. The olfactory channel can be shown to be activated by cyclic nucleotides which leads to a depolarization of olfactory sensory neurons.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel (TC 1.A.1.5) family.

CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.

CC -!- CAUTION: It is uncertain whether Met-1 or Met-2 is the initiator.

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EMBL; U49391; AAC52712.1; -.

MGD; MGI:108040; Cnga2.

GO; GO:0005216; F:ion channel activity; IMP.

GO; GO:0007608; P:olfaction; IMP.

InterPro; IPR000595; cNMP binding.

InterPro; IPR005821; Ion Trans.

InterPro; IPR01622; K+channel pore.

Pfam; PF00027; cNMP binding; 1.

Pfam; PF00520; Ion trans; 1.

SMART; SM00100; cNMP; 1.

PROSITE; PS00888; cNMP BINDING_1; 1.

PROSITE; PS00889; cNMP BINDING_2; FALSE_NEG.

PROSITE; PS0042; cNMP BINDING_3; 1.

ionic channel; Ion transport; CAMP-binding; Transmembrane; Multigene family; Olfaction.

DOMAIN 1 142 CYTOPLASMIC (POTENTIAL).

DOMAIN 143 163 H1 (POTENTIAL).

DOMAIN 164 175 EXTRACELLULAR (POTENTIAL).

DOMAIN 176 194 H2 (POTENTIAL).

DOMAIN 195 218 CYTOPLASMIC (POTENTIAL).

DOMAIN 219 238 H3 (POTENTIAL).

DOMAIN 239 276 EXTRACELLULAR (POTENTIAL).

DOMAIN 277 299 H4 (POTENTIAL).

DOMAIN 300 351 CYTOPLASMIC (POTENTIAL).

DOMAIN 352 371 H5 (POTENTIAL).

DOMAIN 372 455 EXTRACELLULAR (POTENTIAL).

DOMAIN 456 476 H6 (POTENTIAL).

DOMAIN 477 664 CYTOPLASMIC (POTENTIAL).

NP_BIND 464 586 CAMP (BY SIMILARITY).

BINDING 523 538 CAMP (POTENTIAL).

BINDING 538 538 CAMP (POTENTIAL).

CARBOHYD 381 381 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 664 AA; 76209 MW; 90B2601D727C6AFE CRC64;
 Query Match 97.4%; Score 3384; DB 1; Length 664;
 Best Local Similarity 97.6%; Pred. No. 1.9e-218;
 Matches 648; Conservative 3; Mismatches 13; Indels 0; Gaps 0;
 QY 1 MMTKSNVGVKSSPANNHHPSPISKANGKDDHAGSRPQSVAAADDDTSPQLRLAEMDT 60
 Db 1 MMTKSNVGVKSSPANNHHPSPISKANGKDDHAGSRPQSVAAADDDTSPQLRLAEMDT 60
 QY 61 PRRGGRGQRIVRLGVIRWDANKNFRFEEPRDPSFLERFGRPELQTVTHQGGDKGD 120
 Db 61 PRRGGRGQRIVRLGVIRWDANKNFRFEEPRDPSFLERFGRPELQTVTHQGGDKGD 120
 QY 121 GEGGTGKKKFFELFVLDPAGDNYRWLFVIAFVLYNWCLLVARACFSLQRYFVWLV 180
 Db 121 GEGGTGKKKFFELFVLDPAGDNYRWLFVIAFVLYNWCLLVARACFSLQRYFVWLV 180
 QY 181 DYFSDTVVIADLIIRLTGFEQGLLVKDPKLRDNYHTLOFKLDVASIITPTDLYFAV 240
 Db 181 DYFSDTVVIADLIIRLTGFEQGLLVKDPKLRDNYHTLOFKLDVASIITPTDLYFAV 240
 QY 241 GIHSPEVRNKLHFAFMFEFFDRTETSTSPNFRISNLVLYLVIHWNACIYVYISK 300
 Db 241 GIHSPEVRNKLHFAFMFEFFDRTETSTSPNFRISNLVLYLVIHWNACIYVYISK 300
 QY 301 SIGFGVDTWYPNITDPEYGVLAKEYIYCLYWSLTTLTIGETPPPVKDEYLFVDFL 360
 Db 301 SIGFGVDTWYPNITDPEYGVLAKEYIYCLYWSLTTLTIGETPPPVKDEYLFVDFL 360
 QY 361 IGVLIFFATIVGVNISMNNNATAEFOAKIDAVKHYMQFRKVKSKDEAKVIKWFYDWT 420
 Db 361 IGVLIFFATIVGVNISMNNNATAEFOAKIDAVKHYMQFRKVKSKDEAKVIKWFYDWT 420
 QY 421 NKKTVDREVLKNLPAKLRALINHLSTLTKVRIQDMEAGLLVELVLRPQVPSG 480
 Db 421 NKKTVDREVLKNLPAKLRALINHLSTLTKVRIQDMEAGLLVELVLRPQVPSG 480
 QY 481 DYTCKRGDICKEMVYIHEKGLAVVADGVTQYALLSAGSCFGEISILNIKSKMGNRTA 540
 Db 481 DYTCKRGDICKEMVYIHEKGLAVVADGVTQYALLSAGSCFGEISILNIKSKMGNRTG 540
 QY 541 NIRSGLYSDDLFCLSKDDLEAVTEADPAKVLBERGHEILMKGLDENEVAASMEVDVQ 600
 Db 541 TIRSLGYSDDLFCLSKDDLEAVTEADPAKVLBERGHEILMKGLDENEVAASMEVDVQ 600
 QY 601 EKLQLETNMDTHYTRFARLLAETGAQQLKQRTVLETKMKONHEDDVLSDGINTPEP 660
 Db 601 EKLQLETNMDTHYTRFARLLAETGAQQLKQRTVLETKMKONHEDDVLSDGINTPEP 660
 QY 661 TRAE 664
 Db 661 AVAE 664
 RESULT 3
 CN2_RABIT STANDARD; PRT; 664 AA.
 AC Q28718;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cyclic-nucleotide-gated olfactory channel (Cyclic-nucleotide-gated
 cation channel 2) (CNG channel 2) (CNG-2) (CNG2) (Aorta CNG channel)
 DE (RACNG).
 GN CNG2 OR CNGC2.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Aorta;

RX MEDLINE=93359035; PubMed=7689061;
 RA Biel M., Altenhofen W., Hulin R., Ludwig J., Freichel M.,
 R Flokerzi V., Dascal N., Kaupp U.B., Hofmann F.;
 RT "Primary structure and functional expression of a cyclic nucleotide-
 gated channel from rabbit aorta.";
 RL FEBS Lett. 329:134-138(1993).
 CC -!- FUNCTION: Odorant signal transduction is probably mediated by a G-
 protein coupled cascade using cAMP as second messenger. The
 olfactory channel can be shown to be activated by cyclic
 nucleotides which leads to a depolarization of olfactory sensory
 neurons.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
 (TC 1.A.1.5) family.
 CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
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 CC -----
 CC EMBL; X59668; CAA42201.1; ALT INIT.
 DR InterPro; IPR000595; cNMP_binding.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR001622; K_channel_pore.
 DR Pfam; PF00027; cNMP_binding; 1.
 DR Pfam; PF00520; ion_trans; 1.
 DR SMART; SM00100; cNMP; 1.
 DR PROSITE; PS00888; cNMP_BINDING_1; 1.
 DR PROSITE; PS00889; cNMP_BINDING_2; 1.
 DR PROSITE; PS00842; cNMP_BINDING_3; 1.
 DR KW Ionic channel; Ion transport; cAMP-binding; Transmembrane;
 KM Multigene family; Olfaction.
 FT DOMAIN 1 140 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 141 160 H1 (POTENTIAL).
 FT DOMAIN 161 173 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 174 192 H2 (POTENTIAL).
 FT DOMAIN 193 216 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 217 236 H3 (POTENTIAL).
 FT DOMAIN 237 274 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 275 297 H4 (POTENTIAL).
 FT DOMAIN 298 349 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 350 369 H5 (POTENTIAL).
 FT DOMAIN 370 453 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 454 474 H6 (POTENTIAL).
 FT DOMAIN 475 664 CYTOPLASMIC (POTENTIAL).
 FT NP_BIND 462 584 CAMP (BY SIMILARITY).
 FT BINDING 521 521 CAMP (POTENTIAL).
 FT BINDING 536 536 CAMP (POTENTIAL).
 FT CARBOHYD 379 379 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 664 AA; 76205 MW; 5E9170D0B322B3E9 CRC64;

Query Match 93.0%; Score 3231.5; DB 1; Length 664;
 Best Local Similarity 93.8%; Pred. No. 2.9e-208;
 Matches 622; Conservative 16; Mismatches 24; Indels 1; Gaps 1;
 QY 2 MTEKSNVGVKSSPANNHHPSPISKANGKDDHAGSRPQSVAAADDDTSPQLRLAEMDT 61
 Db 1 MTEKSNVGVKSSPANNHHPSPISKANGKDDHAGSRPQSVAAADDDTSPQLRLAEMDT 59
 QY 62 PRRGGRGQRIVRLGVIRWDANKNFRFEEPRDPSFLERFGRPELQTVTHQGGDKGD 121
 Db 60 QRRGGRFRIIVRLGVIRQWANNFRFEEPRDPSFLERFGRPELQTVTHQGGDKGD 119
 QY 122 EGKGTGKKKFFELFVLDPAGDNYRWLFVIAFVLYNWCLLVARACFSLQRYFVWLV 181
 Db 120 DGKGTGKKKFFELFVLDPAGDNYRWLFVIAFVLYNWCLLVARACFSLQRYFVWLV 179
 QY 182 YFSDTVVIADLIIRLTGFEQGLLVKDPKLRDNYHTLOFKLDVASIITPTDLYFAV 241

Db 180 YFSVVVYIADLFIRLTGTGFEQGLLVKDPKLRDNYIHTLQFKLDVASIIPDTLIYFVAVG 239
 QY 242 IHSPEVRENLHFAFMFEFFDRTERTSYVNIERSNLVLYLVIHWNACIYVVISKS 301
 Db 240 IHNPELRFNLLHFAFMFEFFDRTERTSYVNIERSNLVLYLVIHWNACIYVVISKS 299
 QY 302 IGFVDVTWVYVNIPTDPEYCYLAREYIYCLYWSLTLTITIGETPPPVKDEYLVFIYDFELI 361
 Db 300 IGFVDVTWVYVNIPTDPEYCYLAREYIYCLYWSLTLTITIGETPPPVKDEYLVFIYDFELI 359
 QY 362 GVLIFATIVGVNISMNNATRAEFOAKIDAVKHYMQPRKYSKOWEAKVIKWFYDLMTN 421
 Db 360 GVLIFATIVGVNISMNNATRAEFOAKIDAVKHYMQPRKYSKOWEAKVIKWFYDLMTN 419
 QY 422 KKTVDEREVLKLPKAKRAEIAINVHLSLTKKVRIFQDWEAGLLVVLKLRPOVPSGD 481
 Db 420 KKTVDEREVLKLPKAKRAEIAINVHLSLTKKVRIFQDWEAGLLVVLKLRPOVPSGD 479
 QY 482 YICRGDGTGKEMIIKGLAVVADGVQYALLSAGSCFGEISILNKGSKWGNRRATAN 541
 Db 480 YICRGDGTGKEMIIKGLAVVADGVQYALLSAGSCFGEISILNKGSKWGNRRATAN 539
 QY 542 IRLSGVSDLFCLSKDLMKAVTEADPAKVLBERGREILMKGLDENEVAASMEVDVQVE 601
 Db 540 IRLSGVSDLFCLSKDLMKAVTEADPAKVLBERGREILMKGLDENEVAASMEVDVQVE 599
 QY 602 KLEQLETNMTLYTRFARLLAETYGAAQKLKQRIIVLEVKMKONHEDDVLSDGINTPEPT 661
 Db 600 KLEQLETNMTLYTRFARLLAETYGAAQKLKQRIIVLEVKMKONHEDDVLSDGINTPEPT 659
 QY 662 AAE 664
 Db 660 AAE 662

RESULT 4
 CNG2_BOVIN STANDARD; PRT; 663 AA.
 AC Q03041;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cyclic-nucleotide-gated olfactory channel (Cyclic-nucleotide-gated
 DE cation channel 2) (CNG channel 2) (CNG-2) (CNG2).
 GN CNGA2 OR CNCG2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory epithelium;
 RX MEDLINE=91032022; PubMed=1699793;
 RA Ludwig J., Margalit T., Eismann E., Lancet D., Kaupp U.B.;
 RT "Primary structure of CAMP-gated channel from bovine olfactory
 RT epithelium.";
 RL FEBS Lett. 270:24-29 (1990).
 CC -!- FUNCTION: Odorant signal transduction is probably mediated
 CC by a G-protein coupled cascade using cAMP as second messenger.
 CC The olfactory channel can be shown to be activated by cyclic
 CC nucleotides which leads to a depolarization of olfactory
 CC sensory neurons.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Olfactory neurons.
 CC -!- MISCELLANEOUS: The olfactory channel is activated by both cAMP and
 CC cGMP at similar concentrations, whereas the cGMP-gated channel is
 CC much less sensitive to cAMP.
 CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
 CC (TC 1.A.1.5) family.
 CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X55010; CAA38754.1; -.
 CC PIR; S11521; S11521.
 CC InterPro; IPR00595; cNMP_binding.
 CC InterPro; IPR005821; Ion Trans.
 CC InterPro; IPR001622; Kchannel_pore.
 CC Pfam; PF00027; cNMP_binding; 1.
 CC Pfam; PF00520; Ion_Trans; 1.
 CC SMART; SM00100; cNMP; 1.
 CC PROSITE; PS00888; cNMP_BINDING_1; 1.
 CC PROSITE; PS00889; cNMP_BINDING_2; 1.
 CC PROSITE; PS0042; cNMP_BINDING_3; 1.
 CC Ionic channel; Ion transport; CAMP-binding; Transmembrane;
 CC Multigene family; Olfaction; Glycoprotein.
 CC DOMAIN 1 140
 CC TRANSMEM 141 160 H1 (POTENTIAL).
 CC DOMAIN 161 173 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 174 192 H2 (POTENTIAL).
 CC DOMAIN 193 216 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 217 236 H3 (POTENTIAL).
 CC DOMAIN 237 274 H4 (POTENTIAL).
 CC TRANSMEM 275 297 EXTRACELLULAR (POTENTIAL).
 CC DOMAIN 298 349 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 350 369 H5 (POTENTIAL).
 CC DOMAIN 370 453 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 454 474 H6 (POTENTIAL).
 CC DOMAIN 475 663 CYTOPLASMIC (POTENTIAL).
 CC NP_BIND 462 584 CAMP (BY SIMILARITY).
 CC BINDING 521 521 CAMP (BY SIMILARITY).
 CC BINDING 536 536 CAMP (BY SIMILARITY).
 CC CARBOHYD 379 379 N-LINKED (GLCNAC...) (PROBABLE).
 CC SEQUENCE 663 AA; 76014 MW; AB66D4F9203844EF CRC64;
 Query Match 92.2%; Score 3204.5; DB 1; Length 663;
 Best Local Similarity 92.3%; Pred. No. 1.8e-206;
 Matches 610; Conservative 27; Mismatches 23; Indels 1; Gaps 1;
 QY 2 MTEKNGVKSPANNHHPSPISKANGKDDHAGSRPQSVAAADDTSPELQRIAEADTP 61
 Db 1 MTEKANGVKSPANNHHPAIPAKSGKDDHRASSRPQSAAD-DTSSSELQQLAEMDAP 59
 QY 62 RRGGRGGFQRIYVRLVGVIRDWANKNFRERPRPDSFLERERGPPELQVTTTHQDGGKGGK 121
 Db 60 QQRGGGFRIRARLVGVLRWAYNFRERPRPDSFLERFRGPPELHTVTTQQDGGKGGK 119
 QY 122 EGKGTKKKFFELFVLDPAQDWYRMLFVIAMPVLYNCLLVARACFSDLQRYFVWMLVLD 181
 Db 120 EGKGTKKKFFELFVLDPAQDWYRMLFVIAMPVLYNCLLVARACFSDLQRYFVWMLVLD 179
 QY 182 YFSDTVYIADLIIRLTGFEQGLLVKDPKLRDNYIHTLQFKLDVASIIPDTLIYFVAVG 241
 Db 180 YVSDVYIADLIIRLTGFEQGLLVKDPKLRDNYIHTLQFKLDVASIIPDTLIYFVAVG 239
 QY 242 IHSPEVRENLHFAFMFEFFDRTERTSYVNIERSNLVLYLVIHWNACIYVVISKS 301
 Db 240 IHNPEVRENLHFAFMFEFFDRTERTSYVNIERSNLVLYLVIHWNACIYVVISKS 299
 QY 302 IGFVDVTWVYVNIPTDPEYCYLAREYIYCLYWSLTLTITIGETPPPVKDEYLVFIYDFELI 361
 Db 300 IGFVDVTWVYVNIPTDPEYCYLAREYIYCLYWSLTLTITIGETPPPVKDEYLVFIYDFELI 359
 QY 362 GVLIFATIVGVNISMNNATRAEFOAKIDAVKHYMQPRKYSKOWEAKVIKWFYDLMTN 421
 Db 360 GVLIFATIVGVNISMNNATRAEFOAKIDAVKHYMQPRKYSKOWEAKVIKWFYDLMTN 419
 QY 422 KKTVDEREVLKLPKAKRAEIAINVHLSLTKKVRIFQDWEAGLLVVLKLRPOVPSGD 481

Db 420 KKSVDREVLNPKLPAKRAEIAINVHLSTLKKVRFQDCEAGLLVELVLRPQVSPGD 479
 QY 482 YICRKDGIGKEMYYIIKEGKLAVVADGVTQVALLSAGSCFGEISILNKGSGMGNRTAN 541
 Db 480 YICRKDGIGKEMYYIIKEGKLAVVADGVTQVALLSAGSCFGEISILNKGSGMGNRTAN 539
 QY 542 IRSIGYSDFCLSKDDLMMEATVTEAPDAKKVLEERGREILMKMGLDENEVAASMEVDVQE 601
 Db 540 IRSIGYSDFCLSKDDLMMEATVTEAPDAKKVLEERGREILMKMGLDENEVAASMEVDVQE 599
 QY 602 KLEQLETNMDTLTRFARLLAEYTGAAQKLQRIITVLETKMKQNHDDYLSGINTPPT 661
 Db 600 KLEQLETNMDTLTRFARLLAEYTGAAQKLQRIITVLETKMKQNHDDYLSGINTPPT 659
 QY 662 A 662
 Db 660 A 660

RESULT 5

CNG1_CHICK STANDARD; PRT; 735 AA.
 AC Q90805;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cyclic nucleotide-gated channel, cone photoreceptor, alpha subunit
 DE (CNG channel 1) (Chiken-1).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]

SEQUENCE FROM N. A.

RX MEDLINE=93264082; PubMed=7684234;
 RA Boenigk W., Altenhofen W., Mueller F., Dose A., Illing M.,
 RA Molday R.S., Kaupp U.B.;
 RT "Rod and cone photoreceptor cells express distinct genes for
 cGMP-gated channels.";
 RL Neuron 10:865-877(1993).
 CC -!- FUNCTION: Visual signal transduction is mediated by a G-protein
 coupled cascade using cGMP as second messenger. This protein can
 be activated by cyclic GMP which leads to an opening of the cation
 channel and thereby causing a depolarization of cone
 photoreceptors.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
 (TC 1.A.1.5) family.
 CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.

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EMBL; X89598; CAA61757.1; -
 PIR; I50630; I50630.
 DR InterPro: IPR000595; cNMP binding.
 DR InterPro: IPR005821; Ion_trans.
 DR InterPro: IPR001622; K+channel_pore.
 DR Pfam; PF00027; cNMP binding; 1.
 DR Pfam; PF00520; ion_trans; 1.
 DR SMART; SM00100; cNMP; 1.
 DR PROSITE; PS00888; C_NMP_BINDING_1; 1.
 DR PROSITE; PS00889; C_NMP_BINDING_2; 1.
 DR PROSITE; PS00442; C_NMP_BINDING_3; 1.
 KW Ionic channel; Ion transport; cAMP-binding; Transmembrane; Vision;
 Multigene family.
 DOMAIN 1 210 CYTOPLASMIC (POTENTIAL).
 FT

FT	TRANSMEM	211	230	H1 (POTENTIAL).
FT	DOMAIN	231	243	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	244	262	H2 (POTENTIAL).
FT	DOMAIN	263	286	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	287	306	H3 (POTENTIAL).
FT	DOMAIN	307	344	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	345	367	H4 (POTENTIAL).
FT	DOMAIN	368	419	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	420	439	H5 (POTENTIAL).
FT	DOMAIN	440	523	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	524	544	H6 (POTENTIAL).
FT	DOMAIN	545	735	CYTOPLASMIC (POTENTIAL).
FT	NP_BIND	532	654	CAMP (BY SIMILARITY).
FT	BINDING	591	591	CAMP (POTENTIAL).
FT	BINDING	606	606	CAMP (POTENTIAL).
FT	CARBOHYD	449	449	N-LINKED (GLCNAC..) (POTENTIAL).
SQ	SEQUENCE	735 AA;	85031 MW;	A67ADFDD942CFCE CRC64;

Query Match 63.9%; Score 2219.5; DB 1; Length 735;
 Best Local Similarity 59.4%; Pred. No. 1.2e-140;
 Matches 432; Conservative 93; Mismatches 113; Indels 89; Gaps 7;

QY	16	NHNEHPPP	-----SIKANGKDDHRAGS-----RPQSVAAADDDTSPELQRLAEMD-----	59
Db	5	NTQHSYEGMGLSVRTTDEDEIERIENGFIHSLC--EDTSSELQRVISMGRHLSGQT	62	
QY	60	TPRGRGGFORIVLVGVIRDWANKNFRPEEPDPSFLERFGPELQTVTTVTHQ	113	
Db	63	SPFTGRGAMARLSRFVSVLSRWATRLHHDQRPDSFLERIRGPELVEVSSRQNSRFL	122	
QY	114	-----	-----D	114
Db	123	GIREPQGVNWPPLARFNVNFNNNTNEDKKEKKEVKEEKEEKEKDDKDD	182	
QY	115	DKGGKDEGKGTKKXFEFLVDLPAGDWYVFWLFWIAMPVLYNCLLVARACFDLQRYNF	174	
Db	183	KKDDKKDDKKBEQKKEVFVIDPSSNNYNNWLTIIAIPFYNWMLICRACFDELQIDHI	242	
QY	175	VWLVLDYSDTYIADLIIRLTGTFLEQGLLVKDPKRDNYIHTLQFKLDVASIPTD	234	
Db	243	KLWLFYDCSDIIVDFDMFVFRFTGFEQGLLVKDEKLRDHYTQVQKDLVLSLPTD	302	
QY	235	LIYFAVGIIHSPVRENRLHFAWMFEEDTERTTSVPNIERISNLVLIIVHWNACI	294	
Db	303	LAYLKLGLNYPELRFNRLRIARLEFFDRTTRTNYPNNFRIGNLVLYLIIHWNACI	362	
QY	295	YVVISKSGFVDVTWYYPNITDPEYGLAREYIYCLYNSTLTTLTTTGETPPPVKDEYLF	354	
Db	363	YFAISKVIGFGTDSWYYPNVSIPEYGRLSKRYIYSLYNSTLTTLTTTGETPPPVKDEYLF	422	
QY	355	VIFDELIGVLIIFATIVGVNVSIMNNATPAEFOAKIDAVKHMOFPRKYSKDEAKVIKW	414	
Db	423	VVIDLVGLVLIIFATIVGVNVSIMNNASRAEFOAKIDAVKHMOFPRKYSKDEAKVIKW	482	
QY	415	FQYLTWNKKTVDEREVLKOLPAKLAETAINVHLSLTLLKKVRFQDCEAGLLVELVLRPQ	474	
Db	483	FQYLTWNKKTVDEREVLKOLPAKLAETAINVHLSLTLLKKVRFQDCEAGLLVELVLRPQ	542	
QY	475	QVFSFGDYICRKDGIGKEMYYIIKEGKLAVVADGVTQVALLSAGSCFGEISILNKGSGM	534	
Db	543	TVFSPGDYICKGDIGREMYIIKEGKLAVVADGVTQVALLSAGSCFGEISILNKGSGM	602	
QY	535	GNRRTANIRSGYSDLFCLSKDDLMMEATVTEAPDAKKVLEERGREILMKMGLDENEVAAS	594	
Db	603	GNRRTANIRSGYSDLFCLSKDDLMMEATVTEAPDAKKVLEERGREILMKMGLDENEVAAS	662	
QY	595	ME-VDVQEKLEOLETNDTLTRFARLLAEYTGAAQKLQRIITVLETKMKQNHDDYLSG	653	
Db	663	ADPKDLEKIDRLTALDTLQTRFARLLAEYSSSQKQKQRLARVETRVKK-----YSGG	717	
QY	654	GINTPEP	660	
Db	718	SLSVGE	724	

RESULT 6

CNG3_MOUSE
ID CNG3_MOUSE STANDARD; PRT; 631 AA.
AC Q9JZ8; Q9WV01;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cyclic-nucleotide-gated cation channel alpha 3 (CNG channel alpha 3)
DE (CNG-3) (CNG3) (Cyclic nucleotide-gated channel alpha 3) (Cone
DE photoreceptor cGMP-gated channel alpha subunit).
GN CNG3 OR CNG3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Retina;
RX MEDLINE=20273944; PubMed=10813773;
RA Harano A.A., Hack I., Waesle H., Duvoisin R.M.;
RT "Cloning and immunocytochemical localization of a cyclic nucleotide-
RT gated channel alpha-subunit to all cone photoreceptors in the mouse
RT retina.";
RL J. Comp. Neurol. 421:80-94 (2000).
RP [2]
RP SEQUENCE OF 95-631 FROM N.A.
RC STRAIN=129/Sv;
RX MEDLINE=99307448; PubMed=10377453;
RA Biel M., Seeliger M., Pfeifer A., Kohler K., Gerstner A., Ludwig A.,
RA Jaisle G., Fauser S., Zrenner E., Hofmann F.;
RT "Selective loss of cone function in mice lacking the cyclic
RT nucleotide-gated channel CNG3.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:7553-7557 (1999).
CC -1- FUNCTION: Visual signal transduction is mediated by a G-protein
CC coupled cascade using cGMP as second messenger. This protein can
CC be activated by cyclic GMP which leads to an opening of the cation
CC channel and thereby causing a depolarization of cone
CC photoreceptors.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Prominently expressed in retina.
CC -1- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
CC (TC 1.A.1.5) family.
CC -1- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
CC
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CC
CC EMBL; AJ243933; CAB89685.1; -;
CC EMBL; AJ238239; CAB42891.1; -;
CC EMBL; AJ238240; CAB42891.1; JOINED.
CC EMBL; AJ238241; CAB42891.1; JOINED.
CC MGD; MGI:1341818; Cng3a3.
CC GO; GO:0005221; F:intracellular cyclic nucleotide activated c...; IPI.
CC InterPro; IPR000595; cNMP binding.
CC InterPro; IPR005821; Ion Trans.
CC Pfam; PF00027; cNMP binding; 1.
CC Pfam; PF00520; ion Trans; 1.
CC SMART; SM00100; cNMP; 1.
CC PROSITE; PS00888; cNMP BINDING 1; 1.
CC PROSITE; PS00889; cNMP BINDING 2; 1.
CC PROSITE; PS00442; cNMP BINDING 3; 1.
CC Ionic channel; Ion transport; CAMP-binding; Transmembrane;
KW Multigene family; Vision.
FT TRANSMEM 112 133 POTENTIAL.
FT TRANSMEM 244 264 POTENTIAL.

FT TRANSMEM 320 340 POTENTIAL.
FT NP_BIND 423 546 CAMP.
FT BINDING 490 490 CAMP (POTENTIAL).
FT BINDING 505 505 CAMP (POTENTIAL).
FT CONFLICT 110 110 C -> Y (IN REF. 2).
FT CONFLICT 157 157 L -> V (IN REF. 2).
SQ SEQUENCE 631 AA; 72641 MW; 4FA8CD3B9AA3FE6C CRC64;

Query Match 61.9%; Score 2151.5; DB 1; Length 631;
Best Local Similarity 66.8%; Pred. No. 3.5e-136;
Matches 411; Conservative 85; Mismatches 94; Indels 25; Gaps 5;

QY 57 EMDTPRRGRGGFORIVELGVIRDWANKFNREEPRPDSLEPRGDELQVTHQ---- 112
DB 24 DLQHVENG--RVSELLIISIRAWASHUHUDEQDPDSFLDRPHSGSELKEVSTRESNAQ 80
QY 113 ---GDDKGGKGGKGTFFELFVLDPAAGDWTYRMLFVIAMFVLYNWCLLVARACFSDL 169
DB 81 PNPGEQKPPDGGEG---RKEEPIVVDPSNIIYCRMLTALTAIFVYNWCLLVCRACFDEL 136
QY 170 QRYNFFVVLVDYFSDTVYIADLIIRLTGFLQGLLVDPKPKLRDNYIHTLOFKLDVAS 229
DB 137 QSHLTLWLVLVDYSADVLYVLDLVRARTGFLQGLMVRDTKGLKHYYTKTLHFKLDILS 196
QY 230 IIPTDLIYFAVGHISPEVRFNRLHFARMPFEDRTETRTSYENIPIRISNLVLYIIVIH 289
DB 197 LIPTDLAYLKLGVNYPELFRNLKFSRLEFFEDRTETRTSYENIPIRISNLVLYIIVIH 256
QY 290 WNAIYIVTSKSGFGVDTWVYFNITDPEYGLAREYIYCLYWSLTLLTIGETPPPVKD 349
DB 257 WNAIYFAISKFTGFGTDSWYFNITDPEYGLAREYIYCLYWSLTLLTIGETPPPVKD 316
QY 350 EYLFVIFDPLGLVLFATVGNVSGMISNMNATRAEFOAKIDAVKHYNQFRKVSQMEA 409
DB 317 EYLFVIFDPLGLVLFATVGNVSGMISNMNATRAEFOAKIDAVKHYNQFRKVSQMEA 376
QY 410 KVIMKFDYLTNKKTVDEREVLNKLPAKLAETAINVHLSTLKKVIRIFODWAGLLEVLV 469
DB 377 RVIRFDYLTNKKTVDEREVLNKLPAKLAETAINVHLSTLKKVIRIFODWAGLLEVLV 436
QY 470 LKLRQVSPFGYICKGDIKEMWIIKGLKLVAVDDGVTQVALISAGSCFGEISILNI 529
DB 437 LKLRQVSPFGYICKGDIKEMWIIKGLKLVAVDDGVTQVALISAGSCFGEISILNI 496
QY 530 KGSKNMNRRTANIRSLGYSDFCLSKDDLMVAETAPDAKKVLEGRGRLIMKGLDEN 589
DB 497 KGSKNMNRRTANIRSLGYSDFCLSKDDLMVAETAPDAKKVLEGRGRLIMKGLDEN 556
QY 590 EYVAASMEV-DVOEKLEQLETNMDTLYTRFARLLAEYTGAAQKIKORITVLETKM----- 642
DB 557 LVAAARVDRDVEKVEYLESSLDIQTFRFARLLAEYSASQMKLKORLTFLESQMMNRCCG 616
QY 643 ----KQNEHEDDYLSD 653
DB 617 FSPDRENSSEDASKTD 631

RESULT 7
CNG3_BOVIN
ID CNG3_BOVIN STANDARD; PRT; 706 AA.
AC Q29441;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cyclic-nucleotide-gated cation channel alpha 3 (CNG channel alpha 3)
DE (CNG-3) (CNG3) (Cyclic nucleotide-gated channel alpha 3) (Cone
DE photoreceptor cGMP-gated channel alpha subunit).
GN CNG3 OR CNG3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;

```

RN 101 SEQUENCE FROM N.A.
RP TISSUE=Testis;
RC MEDLINE=94211295; PubMed=7512693;
RA Weyand I., Godde M., Frings S., Weiner J., Mueller F., Altenhofen W.,
PA Hat H., Kaupp U.B.;
RT "Cloning and functional expression of a cyclic-nucleotide-gated
RL channel from mammalian sperm.";
RN Nature 368:859-863(1994).
[2]
RN 102 SEQUENCE FROM N.A.
RP TISSUE=Kidney;
RC MEDLINE=94224768; PubMed=8170936;
RA Biel M., Zong X., Distler M., Bosse E., Klugbauer N., Murakami M.,
PA Flockerzi V., Hofmann F.;
RT "Another member of the cyclic nucleotide-gated channel family,
RL expressed in testis, kidney, and heart.";
RN Proc. Natl. Acad. Sci. U.S.A. 91:3505-3509(1994).
CC 1- FUNCTION: Could be responsible for cGMP-induced calcium entry in
CC cells other than sensory cells. Might be involved in chemotaxis of
CC sperm.
CC 2- SUBUNIT: Forms functional heterooligomeric channels with CNG4 in
CC vitro.
CC 3- SUBCELLULAR LOCATION: Integral membrane protein.
CC 4- TISSUE SPECIFICITY: Testis, kidney, retinal cone and heart.
CC 5- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
CC (TC 1.A.1.5) family.
CC 6- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
CC
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CC
CC -----
CC EMBL; X89600; CAA61759.1; -.
CC EMBL; X76485; CAA54023.1; -.
CC PIR; A55251; A55251.
CC InterPro; IPR000595; cNMP binding.
CC InterPro; IPR005821; Ion Trans.
CC InterPro; IPR001622; K-channel_pore.
CC Pfam; PF00027; cNMP_binding; 1.
CC Pfam; PF00520; ion_trans; 1.
CC SMART; SM00100; cNMP; 1.
CC PROSITE; PS00888; cNMP_BINDING_1; 1.
CC PROSITE; PS00889; cNMP_BINDING_2; 1.
CC PROSITE; PS50042; cNMP_BINDING_3; 1.
CC Ionic channel; Ion transport; cAMP-binding; Transmembrane;
CC Multigene family; Vision.
CC TRANSMEM 186 206 POTENTIAL.
CC TRANSMEM 322 342 POTENTIAL.
CC TRANSMEM 398 418 POTENTIAL.
CC NP_BIND 501 624 CAMP.
CC BINDING 568 568 CAMP (POTENTIAL).
CC BINDING 583 583 CAMP (POTENTIAL).
CC SEQUENCE 706 AA; 81132 MW; F4990DCD29B56239 CRC64;
CC
CC Query Match
CC Best Local Similarity 61.6%; Score 2140; DB 1; Length 706;
CC Matches 419; Conservative 94; Mismatches 119; Indels 62; Gaps 7;
CC
CC 11 SSPANNHHPPPSKANGK-DHRRAGRPQSVADDDTSPQLQFLAEMDTFRGRG--- 66
CC 9 SHPTRTH-----PSVRTMDRLDCIENGLSRTHLPCEITSSELQEGIANET--RGLAESR 61
CC
CC 67 -----GFQIRVLGVIRWANKNFREPRDPSFLERGRPBLQVTHQG----- 113
CC 62 QSSFTSQGPTRLSLRLISLRAWSARHLHQDQRDPSFLERFRGALQELQVSSRSVHQPNU 121
CC
CC 114 -----DDKGGKDG-----GKGTKKKFLFVLD 136

```

RESULT 8

CNG3_HUMAN

ID_CNG3_HUMAN

STANDARD;

PRT; 694 AA.

Q16281; Q9UP64;

01-NOV-1997 (Rel. 35, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

15-MAR-2004 (Rel. 43, last annotation update)

Cyclic-nucleotide-gated cation channel alpha 3 (CNG channel alpha 3)

Cyclic-nucleotide-gated cation channel alpha 3 (CNG channel alpha 3)

Cyclic-nucleotide-gated cation channel alpha 3 (CNG channel alpha 3)

Cyclic-nucleotide-gated cation channel alpha 3 (CNG channel alpha 3)

Cyclic-nucleotide-gated cation channel alpha 3 (CNG channel alpha 3)

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Cyclic-nucleotide-gated cation channel alpha 3 (CNG channel alpha 3)

Cyclic-nucleotide-gated cation channel alpha 3 (CNG channel alpha 3)

Cyclic-nucleotide-gated cation channel alpha 3 (CNG channel alpha 3)

RA Kohl S., Marx T., Giddings I., Jaegle H., Jacobson S.G.,
 RA Apfelstedt-Syllia E., Zrenner E., Sharpe L.T., Wässinger B.;
 RT "Total colourblindness is caused by mutations in the gene encoding the
 RT alpha-subunit of the cone photoreceptor cGMP-gated cation channel.";
 RL Nat. Genet. 19:257-259 (1998).
 CC -!- FUNCTION: Visual signal transduction is mediated by a G-protein
 CC coupled cascade using cGMP as second messenger. This protein can
 CC be activated by cyclic GMP which leads to an opening of the cation
 CC channel and thereby causing a depolarization of cone
 CC photoreceptors.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Prominently expressed in retina.
 CC -!- DISEASE: Defects in CNGB3 are a cause of rod monochromacy (RMCH)
 CC [MIM:216900]; also known as total colorblindness or achromatopsia.
 CC RMCH is an autosomal recessively inherited condition.
 CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
 CC (TC 1.A.1.5) family.
 CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
 CC -!- DATABASE: NAMES=Mutations of the CNGB3 gene;
 CC NOTE=Retina International's Scientific Newsletter;
 CC WWW="http://www.retina-international.com/sci-news/cng3mut.htm".
 CC -----
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 CC -----
 DR EMBL; AR065314; AAC17440.1; -.
 DR EMBL; S76069; AAD14208.1; -.
 DR PIR; I78560; I78560.
 DR Genew; HGNC:2150; CNGB3.
 DR MIM; 600053; -.
 DR MIM; 216900; -.
 DR GO; GO:0015276; F:ligand-gated ion channel activity; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR GO; GO:0006810; P:transport; TAS.
 DR GO; GO:0007601; P:vision; TAS.
 DR InterPro; IPR000595; cNMP binding.
 DR InterPro; IPR005821; Ion Trans.
 DR InterPro; IPR001622; K+channel pore.
 DR Pfam; PF00027; cNMP binding; 1.
 DR Pfam; PF00520; Ion trans; 1.
 DR SMART; SM00100; cNMP; 1.
 DR PROSITE; PS00888; CNMP BINDING_1; 1.
 DR PROSITE; PS00889; CNMP BINDING_2; 1.
 DR PROSITE; PS00042; CNMP BINDING_3; 1.
 KW Ionic channel; Ion transport; cAMP-binding; Transmembrane;
 KW Multigene family; Vision; Disease mutation; Polymorphism.
 FT TRANSMEM 171 192 POTENTIAL.
 FT TRANSMEM 305 325 POTENTIAL.
 FT TRANSMEM 378 397 POTENTIAL.
 FT NP_BIND 482 605 CAMP.
 FT BINDING 549 549 CAMP (POTENTIAL).
 FT BINDING 564 564 CAMP (POTENTIAL).
 FT VARIANT 153 153 T -> M.
 FT VARIANT 163 163 /FTid=VAR_010902.
 FT P -> L (in RMCH).
 FT VARIANT 283 283 /FTid=VAR_010903.
 FT R -> Q (in RMCH).
 FT /FTid=VAR_010904.
 FT R -> W (in RMCH).
 FT /FTid=VAR_010905.
 FT T -> R (in RMCH).
 FT /FTid=VAR_010906.
 FT R -> W (in RMCH).
 FT /FTid=VAR_010910.
 FT V -> M (in RMCH).
 FT /FTid=VAR_010907.
 FT F -> L (in RMCH).
 FT /FTid=VAR_010908.

FT VARIANT 557 557 G -> R (in RMCH).
 FT /FTid=VAR_010909.
 SQ SEQUENCE 694 AA; 78838 MW; AE00B4EE760D70A0 CRC64;
 Query Match 61.6%; Score 2139; DB 1; Length 694;
 Best Local Similarity 61.5%; Pred. No. 2.7e-135;
 Matches 429; Conservative 93; Mismatches 129; Indels 46; Gaps 10;
 QY 5 KNGVSSPANNNHHPPSIKANGKDDHRAG---SRQSVAAADDDTSPELQRLAEMDT- 60
 DB 3 KINTQSHPSRTH-----LKVTSDRLNRAENGSLRAHS--SSSETSVLPQGIAMETR 55
 QY 61 --PRGRG-----GFQIRVLGVIRDMANKFREPEPRDSFLERFGPELQTVTHQG 113
 DB 56 GLADSSQGSFTQGIARLSRLIFLLRWAARHVVHQDQGFSPDFRFRGAELKEVSSQS 115
 QY 114 D-----DKG-----GKDGEGKTKKPFELVLDAGWYRFLV 148
 DB 116 NAAQVGSQBPADRGSRSAWPLAKONTNTSNTEEKTKK-DAIVDPSSNLYRKLTA 174
 QY 149 IAMPVLNWCLLVARACFSDLQNTFVVMVLVDYSDTVYIADLIIRLTGFLQGLLVK 208
 DB 175 IALPFYNWLLICRACFDELQSEYLMMLVDYSADVLVLDLVVARTGFLQGLMVS 234
 QY 209 DPKKURDNIHTLQFKLDVASIIPDILYFAGVHSPPEVRNRLHFAKMFPPFDTR 268
 DB 235 DTNRLWQHYKTTTQFKLDVLSVPTDLAYLVGTNYPEVRNRLKFSRLEFPFDTR 294
 QY 269 TSYNIFRISNLVILVLIHWNACIYVYSKISGRVDVTWYVYVNTDPEYGLAREYI 328
 DB 295 TNPNNFRIGNLVLYLIIHWNACIYFALSIFGFGTDSWYIPNISIEHGKLSKYI 354
 QY 329 CLYWSLTTLTIGETPPPVKDEYLFVIFDFELIGLVLFATIVGNVGSMSNNMTRAEFQ 388
 DB 355 SLYWSLTTLTIGETPPPVKDEYLFVVDVFLVGLVLFATIVGNVGSMSNNMTRAEFQ 414
 QY 389 AKIDAVKHMOPRKVKOMEAKVWFDFYLTWNTKTVDEREVLKNIPAKRAEIAINVHL 448
 DB 415 AKIDSIKQYMQFRKVTQLETRVIRWFDYLVANKTVDEKVLKSLPDKRAEIAINVHL 474
 QY 449 STIKKVRIFQDWEAGLVLLKLRQVPSPGDYICRKGDIGKEMVILKEGLAVVADDG 508
 DB 475 DTUKKVRIFQDCEAGLVLLKLRFTVSPGDYICKGDIKEMVINEGLAVVADDG 534
 QY 509 VTQYALLSAGSCFGEISILNIKSGNRRRTANIRSLGYSDFLCLSKDDLMEAVTRAPDA 568
 DB 535 VTQFVVLSDGYPGEISILNIKSGNRRRTANIRSGYSDFLCLSKDDLMEALTEYPEA 594
 QY 569 KKVLEERGHEILMKGLLDENEVAASME-VDVQEKLEQLETNMDTLYTFARLLAEYVGA 627
 DB 595 KKALEEKGRQILMKONLIDELARAGADPDUEKVEQLGSSLDLTQTRFARLLAYNAT 654
 QY 628 QOKLKQRIWLETMKQNEHDDYLSDGINTPEPTAAE 664
 DB 655 QMKMKQRLSQLESQVK-GGGDKPLADGEVPGDATKTE 690
 RESULT 9
 CNG ICTPU STANDARD; PRT; 682 AA.
 AC P55934;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cyclic-nucleotide-gated cation channel.
 OS Ictalurus punctatus (Channel catfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Siluriformes;
 OC Ictaluridae; Ictalurus.
 RN NCBI_TaxID=7998;
 RP [1]
 RP TISSUE=Olfactory neuroepithelium;

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RX MEDLINE=92110008; PubMed=1370374;
RA Goulding E.H., Ngai J., Kramer R.H., Colicos S., Axel R.,
RA Siegelbaum S.A., Chess A.;
RT "Molecular cloning and single-channel properties of the cyclic
RT nucleotide-gated channel from catfish olfactory neurons.";
RL Neuron 8:45-58(1992).
CC -1- FUNCTION: This cyclic nucleotide-gated channel is activated
CC equally well by both cAMP and cGMP.
CC -1- TISSUE SPECIFICITY: Olfactory neurons.
CC -1- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
CC (TC 1.A.1.5) family.
CC -1- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M83111; -; NOT ANNOTATED_CDS.
DR PIR; JH0560; JH0560.
DR InterPro; IPR000595; cNMP_binding.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR001622; K-channel_pore.
DR InterPro; IPR001201; PAP_25A_core.
DR Pfam; PF00027; cNMP_binding; 1.
DR Pfam; PF00520; Ion_trans; 1.
DR SMART; SM00100; cNMP; 1.
DR PROSITE; PS00886; cNMP_BINDING_1; 1.
DR PROSITE; PS00889; cNMP_BINDING_2; 1.
DR PROSITE; PS00442; cNMP_BINDING_3; 1.
DR Olfaction; Ion transport; Ionic channel; cAMP-binding; cGMP-binding;
KW Transmembrane.
KW DOMAIN 1 136 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 137 157 H1 (POTENTIAL).
FT DOMAIN 158 169 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 170 190 H2 (POTENTIAL).
FT DOMAIN 191 218 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 219 239 H3 (POTENTIAL).
FT DOMAIN 240 272 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 273 293 H4 (POTENTIAL).
FT DOMAIN 294 311 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 312 332 H5 (POTENTIAL).
FT DOMAIN 333 343 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 344 364 H6 (POTENTIAL).
FT DOMAIN 365 682 CYTOPLASMIC (POTENTIAL).
FT NP_BIND 455 577 CAMP (BY SIMILARITY).
FT BINDING 514 514 CAMP (POTENTIAL).
FT BINDING 529 529 CAMP (POTENTIAL).
SQ SEQUENCE 682 AA; 78020 MW; 2C78597DC2C74F75 CRC64;
Query Match 61.3%; Score 2131; DB 1; Length 682;
Best Local Similarity 67.7%; Pred. No. 9.1e-135;
Matches 419; Conservative 68; Mismatches 110; Indels 22; Gaps 6;
QY 34 RAGSRPOSVAADDDTSPQLRLAEMDTPR-----RGRGQFQIRVLGVIRDWANKNF 86
DB 28 RAESAISRTDGDGDDTSELQRTALELPSAEMLEAFTQRRPLARLVNLVLSREWAHKS 87
QY 87 REEPRPDSFLERFGPELQVTTHQGDGK--KDGEGKTKKPFVLVDLPAGDWYR 144
DB 88 VETEQRPSFLERFGPQ-----AANDQSAAPADAFKTKFERWEGVYVSQSDDIYY 140
QY 145 WLFVAMPVYNWCLLVARACFSIDQRYFVVWLVLDYFSTVYADLIIRLTGFLBQ 204
DB 141 WLFVIALASLVNWLINWVARACFDQDENFLLWGLVDLCVDYILDTICILRLTYGLEQ 200
QY 205 LLVKDPKKLRDNYIHTLQFKLDVASIITDLYIFAVGHSPEVFNRLHLLHFAFMFEFDR 264
DB 201 LLVKDLAKLRDNYINTLQFKLDFTLSILTELLFFVTG-YVQLRNLRLHLLHFAFMFEFDR 259

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QY 265 TETRTYPNIFRISNLVLYLIIHWNACIYVYVVISKISGFGVDTWVYVFNITDBEYGYLAR 324
DB 260 TETRTYVNAFRICNLILYLVIIHWNACIYVYVVISKISGFGVDTWVYVFNITDBEYGYLAR 315
QY 325 EYIYCYVWSLTLTITGEMPPPKVDEYLFVIFDELIGVLIFATIVGVSGMISNMNATR 384
DB 316 CYVYCFWSTLTITGEMPPPKVDEYLFVIFDELIGVLIFATIVGVSGMISNMNATR 375
QY 385 AEFQAKIDAVKHYMQFKVSKDMEAKVWKVDFYLTWNTKKTVDREVLKKNLPKALRAEIAI 444
DB 376 AEFQTRIDALIKHYMHFKVNRITLTVKWFYLVNTKKTVDREVLKKNLPKALRAEIAI 435
QY 445 NVHLSTLTKVRIQDWEAGLLVELVLKLRQVSPGDYICRKGDIKGMIIKEGKLAVV 504
DB 436 NVHLDTLTKVRIQDWEAGLLVELVLKLRQVSPGDYICRKGDIKGMIIKEGKLAVV 495
QY 505 ADDGVQYALLSAGSCFGEISILNIKSGKMGNRRTANIRSLIGYSDLFCLSKDDLMEAVTE 564
DB 496 ADDGVQYALLSAGSCFGEISILNIKSGKMGNRRTANIRSLIGYSDLFCLSKDDLMEAVTE 555
QY 565 APDAKVLIERGREILMKGLDENEVAASMEV-DVOEKLEQLETNMDTLYTRFARLLAE 623
DB 556 YPDAQVLEERGREILRKQGLDDESVAAAGLGVITDEEKVERLDASLDILQTRFARLLGE 615
QY 624 YTGQVQKLKORITVLETYM 642
DB 616 FTSTQRELKORITALERQL 634
RESULT 10
CNG3_CHICK STANDARD; PRT; 645 AA.
AC Q90980;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cyclic nucleotide gated channel, ROD photoreceptor, alpha subunit
DE (CNG channel 3) (CNG3).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP MEDLINE=93264082; PubMed=7684234;
RX Boenick W., Altenhofen W., Mueller F., Dose A., Illing M.,
RA Molday R.S., Kaupp U.B.;
RT "Rod and cone photoreceptor cells express distinct genes for
RT cGMP-gated channels.";
RL Neuron 10:865-877(1993).
CC -1- FUNCTION: VISUAL SIGNAL TRANSDUCTION IS MEDIATED BY A G-PROTEIN
CC BE ACTIVATED BY CYCLIC GMP WHICH LEADS TO AN OPENING OF THE CATION
CC CHANNEL AND THEREBY CAUSING A DEPOLARIZATION OF ROD
CC PHOTORECEPTORS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
CC (TC 1.A.1.5) family.
CC -1- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
CC -----
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CC -----
CC EMBL; X89599; CAA61758.1; -
DR PIR; I50680; I50680.
DR InterPro; IPR000595; cNMP_binding.
DR InterPro; IPR005821; Ion_trans.

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CC WWW="http://www.retina-international.com/sci-news/cngalmut.htm".
CC -----
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CC -----
DR EMBL; M4741; AAA52010.1; AUT_INIT.
DR EMBL; S42457; AAB22778.1; -.
DR EMBL; S76062; AAD14206.1; -.
DR PIR; A42161; A42161.
DR Genew; HGNC:2148; CNGA1.
DR MIM; 123825; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0006810; P:transport; TAS.
DR GO; GO:0007601; P:vision; TAS.
DR InterPro; IPR000595; cNMP binding.
DR InterPro; IPR005821; Ion Trans.
DR Pfam; PF00027; cNMP_binding; 1.
DR Pfam; PF00520; Ion_Trans; 1.
DR SMART; SM00100; cNMP; 1.
DR PROSITE; PS00888; cNMP_BINDING_1; 1.
DR PROSITE; PS00889; cNMP_BINDING_2; 1.
DR PROSITE; PS50042; cNMP_BINDING_3; 1.
DR Tonic channel; Ion transport; cNMP-binding; Transmembrane;
KW Multigene family; Vision; Disease mutation; Polymorphism;
KW Retinitis pigmentosa.
KN DOMAIN 1 160
FT TRANSEM 161 181
FT DOMAIN 182 194
FT TRANSEM 195 213
FT DOMAIN 214 237
FT TRANSEM 238 257
FT DOMAIN 258 295
FT TRANSEM 296 318
FT DOMAIN 319 370
FT TRANSEM 371 390
FT DOMAIN 391 474
FT TRANSEM 475 495
FT DOMAIN 496 686
FT NP BIND 683 605
FT BINDING 542 542
FT BINDING 557 557
FT CARBOHYD 421 421
FT VARIANT 28 28
FT VARIANT 114 114
FT VARIANT 316 316
FT VARIANT 46 46
FT CONFLICT 85 85
FT CONFLICT 146 147
FT CONFLICT 539 539
FT CONFLICT 677 678
FT SEQUENCE 686 AA; 79126 MW; B5200D216FC97AF6 CRC64;
Query Match 58.5%; Score 2034; DB 1; Length 686;
Best local similarity 61.4%; Pred. No. 2.7e-128;
Matches 403; Conservative 88; Mismatches 135; Indels 30; Gaps 5;
QY 23 PSIKANGKDHGRAGRQPSVAADDTSPLOLRLAEMTPRRGRGF-----ORI 71
DB 21 PDIE---KEIKRMENGACSPFSDDDASTSESENEP-HARGSFYSLRKGPQSQRE 76
QY 72 VRLGVGIR-----DWANKNFRBEEPRPDSFLFRFRGPPELQTVTHQGDGK 117
DB 77 QYLFGAIFLNVNSSNKQDEPEKKKKKKKKSKSDKNKNKNDPEKKKKKKKKKK 136

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QY 118 GKDGEKGTGKKKFFELVDPDAGDWYRMLFVIAMFVLNWCILLVARACFSDIQRYFVW 177
DB 137 BEKSKDKKEEKKEVVVIDPSCNTYNNMFCITLFWNNWTVIARACFDELQSDYLEW 196
QY 178 LVLDFSTVYADLIIRLTGFLBQGLLVDPKPKLRDNYIHTLQFKLDVASILPTDLY 237
DB 197 LLDVSDIVLIDMFVTRTGTGLBQGLLVKELKLNKYKSNLQFKLDVLSLPTDLY 256
QY 238 FAVGTHSPVRNRLHFAFMPEFFDRTETRTSYENIFRISNLVLYLVIHWNACIYV 297
DB 257 FKLGNVYBEIRLNLRLRSRMPEFFQRTETRYNIFRISNLVYVLIHWNACVYS 316
QY 298 ISKISGFGVDWVYNNITDPEYGYLAREYIYCLYWSLTTLTTIGETPPPVKDEYLFVIF 357
DB 317 ISKALGFGNDTWVYDINDPFRGLARKVYVSLYWSLTTLTTIGETPPPVRSYFVVV 376
QY 358 DFLIGVLIFATVGNVSMISNNNATRAEFQAKIDAVKHVMQFRKVSMDKAEKVIKWFY 417
DB 377 DFLIGVLIFATVGNVSMISNNNARAEFQARIIDAIKQIMHFRNVSKDKERKVIKWFY 436
QY 418 LWTNKKTVDEREVLKMLPAKRAEIAINVHLSTLKKVRFQDWEAGLLVVLKLRPQVF 477
DB 437 LWTNKKTVDEKEVLKLPDLKRAEIAINVHLDTLKKVRIFADCEAGLLVVLKLPQVY 496
QY 478 SPGDYICRKGDIGKMYIIKEGLAVVADGVTQVALLSAGSCFGEISILNKGSKGNR 537
DB 497 SPGDYICKKGDIGREMYIIKEGLAVVADGVTQFVVLSDGSYFGEISILNKGSKAGR 556
QY 538 RTANTRSLGYSDLFCLSKDDLMENATEAPDAKVLLEERGRELKMKGLDENEV-AASME 596
DB 557 RTANIKSIGYDLFCLSKDDLMENATEYDPAKMLEEKQKILMKDGLDLNANAGSDP 616
QY 597 VDVQEKLEQLETNMDTLTYRFAALLAEYTGAAQKLRITVLETKMKQNHEDDYL 652
DB 617 KULEKVTMEGSDVLLQTRFARILAEVSMQKQKRLTKVKEFKLPLIDTFSS 672
RESULT 13
CNGI_RAT
ID_CNGI_RAT STANDARD; PRT; 683 AA.
AC O62927; O08659;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-NOV-2004 (Rel. 43, Last annotation update)
DE cGMP-gated cation channel alpha 1 (CNG channel alpha 1) (CNG-1) (CNGI)
DE (Cyclic nucleotide-gated channel alpha 1) (Cyclic nucleotide-gated
DE channel, photoreceptor) (Cyclic-nucleotide-gated cation channel 1)
DE (Rod photoreceptor cGMP-gated channel alpha subunit).
GN CNGA1 OR CNCG1 OR CNCG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Barnstable C.J., Wei J.Y.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97287732; PubMed=9142860;
RA Ding C., Potter E.D., Qiu W., Coon S.L., Levine M.A., Guggino S.E.;
RT "Cloning and widespread distribution of the rat rod-type cyclic
RT nucleotide-gated cation channel.";
RL Am. J. Physiol. 272:CI335-CI344(1997).
RN [3]
RP SEQUENCE OF 521-693 FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=97197878; PubMed=9045728;
RA Bradley J., Zhang Y., Bakin R., Lester H.A., Ronnett G.V., Zinn K.;
RT "Functional expression of the heteromeric 'olfactory' cyclic
RT nucleotide-gated channel in the hippocampus: a potential effector of
RT synaptic plasticity in brain neurons."

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CC CC EMBL; M84742; AAA37425.1; -;
CC CC EMBL; U19717; AAA85702.1; -;
DR DR EMBL; U19715; AAA85700.1; -;
DR DR EMBL; U19716; AAA85701.1; -;
DR DR MGD; MGI:88436; Cngal.
DR DR InterPro; IPR000595; cNMP binding.
DR DR InterPro; IPR005821; Ion Trans.
DR DR InterPro; IPR001622; K+channel_pore.
DR DR Pfam; PF00027; cNMP binding; 1.
DR DR Pfam; PF00520; Ion trans; 1.
DR DR SMART; SM00100; cNMP; 1.
DR DR PROSITE; PS00888; cNMP BINDING_1; 1.
DR DR PROSITE; PS00889; cNMP BINDING_2; 1.
DR DR PROSITE; PS00442; cNMP BINDING_3; 1.
KW Ionic channel; Ion transport; cNMP-binding; Transmembrane;
KW Multigene family; Vision.
KW DOMAIN 1 156 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 157 177 H1 (POTENTIAL).
FT DOMAIN 178 190 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 191 209 H2 (POTENTIAL).
FT DOMAIN 210 233 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 234 253 H3 (POTENTIAL).
FT DOMAIN 254 291 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 292 314 H4 (POTENTIAL).
FT DOMAIN 315 366 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 367 386 H5 (POTENTIAL).
FT DOMAIN 387 470 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 471 491 H6 (POTENTIAL).
FT DOMAIN 492 684 CYTOPLASMIC (POTENTIAL).
FT NP BIND 479 601 CGMP (POTENTIAL).
FT BINDING 538 538 CGMP (POTENTIAL).
FT BINDING 553 553 CGMP (POTENTIAL).
FT CARBOHYD 417 417 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 113 114 NK -> I (IN REF. 1).
FT CONFLICT 200 200 D -> N (IN REF. 1).
FT CONFLICT 576 576 A -> V (IN REF. 1).
FT CONFLICT 635 635 R -> C (IN REF. 1).
FT SEQUENCE 684 AA; 79460 MW; 13E2A405B68CBF CRC64;

Query Match 57.9%; Score 2012.5; DB 1; Length 684;
Best Local Similarity 61.5%; Pred. No. 7.4e-127;
Matches 401; Conservative 87; Mismatches 141; Indels 23; Gaps 6;
QY 21 PPSIKANGKDHRRGSRQSVAAADDTSPQLQLAEMDTPRG-----RGGFQIRVLV 75
Db 16 PNIVFAIEKEIRMEMGACSFSDDDNGSLSESENEFSFRNSYKRRGPSQREQHLP 75
QY 76 GV-----IRDWANK-----FREERPPDSFLERFRGPBLQVTTTHQGD--DKGGK 119
Db 76 GTMALFNVNNSNKQDEPKKKKKKKKKKADKNKKDPEKKKKKKKKKKKKKK 135
QY 120 DGEKGTKKKFELVDLPAGDWTYRMLFVTAMPVLVNWCLLVARCFSDLQRYFVVVLV 179
Db 136 TKEKKEEEKK-EVVVIDPSGNTYNNMLFCITLPMYNNWTMIARACFDELQSDYLEYVLI 194
QY 180 LDYFSDVTYIADLIIRLTGFLGGLVADPKKLRDNYIHTLOPKLDVASIITDLYFA 239
Db 195 FDVSDVVVLADLVFVTRTGLGGLLVKDKMKLIEKYNKALQKGLVLSVIFTDLYIK 254
QY 240 VGHSPVFNRLHLHFAFMFEFFDRTETRTSYNIFRISNLVLIIVIIHWNACIYVVIS 299
Db 255 FGWNPYRILNLLRISRMFEFFORTETRTNYNPIFRISNLVMYVIVIIHWNACVVIS 314
QY 300 KSTGFGVDVTWYVNIIDPEYGLAREIYCLYSLTTLTIGETPPPVKDBEYLVIFDF 359
Db 315 KATGFGNDVTWYVDPNDPEFGRGLARKYVSLYSLTTLTIGETPPPVLDSEYIFVVVDF 374
QY 360 LIGVLIFATVGVNIGSMISNNATRAEFQAKIDAVKHVMOFRKYSKDMKAKVIKWDYLW 419
Db 375 LIGVLIFATVGVNIGSMISNNATRAEFQSRVDAIKQYMMFRNVSKDMKRVIKWEDYLW 434

Search completed: May 12, 2004, 11:14:14
Job time : 19 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 12, 2004, 11:11:05 ; Search time 45 Seconds
(without alignments)
4655.646 Million cell updates/sec

Title: US-10-087-217a-8
Perfect score: 3475
Sequence: 1 WMTXSGVYKSPANNHH.....NHEDDYLSGINTPEPTAAE 664

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25: *
1: sp_archea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mbc: *
8: sp_organelle: *
9: sp_phase: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_rvirus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	3405	98.0	664	11 Q80XH6	Q80XH6 mus musculus
2	2160.5	62.2	631	11 Q8CFV6	Q8CFV6 mus musculus
3	2147.5	61.8	632	11 Q9ER32	Q9ER32 rattus norv
4	2140	61.6	670	11 Q9ER33	Q9ER33 rattus norv
5	2132	61.4	611	11 Q9QWN7	Q9QWN7 rattus norv
6	2035	58.6	686	6 Q9N0H4	Q9N0H4 sus scrofa
7	1927	55.5	637	13 Q80416	Q80416 carassius a
8	1862	53.6	737	13 Q8UVF8	Q8UVF8 oncorhynch
9	1433	41.2	609	13 Q8JFP0	Q8JFP0 ictalurus p
10	1375	39.6	551	13 Q8JFN9	Q8JFN9 ictalurus p
11	1278.5	36.8	474	4 Q8TV77	Q8TV77 homo sapien
12	1180.5	34.0	900	5 Q97119	Q97119 limulus pol
13	1176	33.8	1218	5 Q9W201	Q9W201 drosophila
14	1128	32.5	252	11 Q9QX26	Q9QX26 rattus norv
15	1068	30.7	1463	5 Q9USE2	Q9USE2 drosophila
16	997	28.7	1324	5 Q8IR35	Q8IR35 drosophila

17	997	28.7	1696	5	Q9VXV8	Q9VXV8 drosophila
18	873.5	25.1	695	5	Q93486	Q93486 caenorhabdi
19	870.5	25.1	1037	5	Q9W2D5	Q9W2D5 drosophila
20	870.5	25.1	1040	5	Q8IH43	Q8IH43 drosophila
21	863.5	24.8	832	5	Q9N4C1	Q9N4C1 caenorhabdi
22	835	24.0	800	5	P90975	P90975 caenorhabdi
23	835	24.0	800	5	O62237	O62237 caenorhabdi
24	831	23.9	644	5	O61827	O61827 caenorhabdi
25	784	22.6	866	11	Q80XL8	Q80XL8 mus musculu
26	782	22.5	809	4	Q9NQW8	Q9NQW8 homo sapien
27	778	22.4	1245	4	O43636	O43636 homo sapien
28	778	22.4	1251	4	Q9UMG2	Q9UMG2 homo sapien
29	773.5	22.3	858	11	O55157	O55157 rattus norv
30	773.5	22.3	1339	11	O35788	O35788 rattus norv
31	770	22.2	938	6	O77658	O77658 bos taurus
32	770	22.2	948	6	O77659	O77659 bos taurus
33	770	22.2	952	6	O77660	O77660 bos taurus
34	758.5	21.8	694	11	Q9UJZ9	Q9UJZ9 mus musculu
35	753	21.7	515	5	Q9S5L0	Q9S5L0 drosophila
36	728	20.9	782	6	Q8WJD7	Q8WJD7 canis famil
37	716.5	20.6	610	4	Q9NRE9	Q9NRE9 homo sapien
38	670	19.3	151	11	P70607	P70607 rattus norv
39	550	15.8	605	5	O72205	O72205 caenorhabdi
40	516.5	14.9	767	5	O76977	O76977 stronglyloce
41	511	14.7	890	4	Q86WJ6	Q86WJ6 homo sapien
42	502	14.4	945	5	Q9Y1J9	Q9Y1J9 drosophila
43	502	14.4	1327	5	Q9V702	Q9V702 drosophila
44	501.5	14.4	678	5	O96777	O96777 heliothis v
45	481	13.8	774	4	Q86WJ5	Q86WJ5 homo sapien

ALIGNMENTS

RESULT 1

Q80XH6	ID	Q80XH6	PRELIMINARY;	PRT;	664 AA.
AC	Q80XH6;				
DT	01-JUN-2003 (TtEMBLrel. 24, Created)				
DT	01-JUN-2003 (TtEMBLrel. 24, Last sequence update)				
DT	01-OCT-2003 (TtEMBLrel. 25, Last annotation update)				
DE	Cyclic nucleotide gated channel 4.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Olfactory epithelium;				
RX	MEDLINE=22388257; PubMed=12477932;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Wang J., Haieh F.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E.,				
RA	Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,				
RA	Richards S., Worley K.C., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Whiting M., Madan A., Kettman M., Madan A., Rodriguez S., Sanchez A.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,				
RA	Jones S.J., Marra M.A.,				
RA	"Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences."				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
RP	[2]				
RC	SEQUENCE FROM N.A.				
RC	TISSUE=Olfactory epithelium;				

```

RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC048775; AAH48775.1; -.
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0002216; F.ion channel activity; IEA.
DR GO; GO:0005267; F.potassium channel activity; IEA.
DR GO; GO:0006811; F.ion transport; IEA.
DR GO; GO:0006813; P.potassium ion transport; IEA.
DR InterPro; IPR000595; cNMP binding.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR001821; ion_trans.
DR Pfam; PF00027; cNMP_binding; 1.
DR Pfam; PF00520; ion_trans; 1.
DR SMART; SM00100; cNMP; 1.
DR PROSITE; PS00888; cNMP_BINDING_1; 1.
DR PROSITE; PS00889; cNMP_BINDING_2; 1.
DR PROSITE; PS00042; cNMP_BINDING_3; 1.
SQ SEQUENCE 664 AA; 76192 MW; 34F8DF3B372C0D9C CRC64;

Query Match          98.0%; Score 3405; DB 11; Length 664;
Best Local Similarity 98.2%; Pred. No. 6.5e-244;
Matches 652; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 MMTKSNVGVKSSPANNHHPPPSIKANGKDDHAGSRPOSVAADDDTSPELQRLAEMDT 60
DB 1 MMTKSNVGVKSSPANNHHPPPSIKANGKDDHAGSRPOSVAADDDTSSELQRLAEMDT 60

QY 61 PRRGGGGQFRIVLGVIRDWANKNFREPRDPSFLFRGPELQVTTTHQGDGKGD 120
DB 61 PRRGGGGQFRIVLGVIRDWANKNFREPRDPSFLFRGPELQVTTTHQGDGKGD 120

QY 121 GEGHGTGKKKELFVLDAGDWYRWLFVAMPVLYNWCLLVARACFSDLOQNYFVWLVL 180
DB 121 GEGHGTGKKKELFVLDAGDWYRWLFVAMPVLYNWCLLVARACFSDLOQNYFVWLVL 180

QY 181 DYPGSDTVIADLIIRLTGFEQGLLVKDPKLRDNYHTLOFKLDVASIPTDLYFAV 240
DB 181 DYPGSDTVIADLIIRLTGFEQGLLVKDPKLRDNYHTLOFKLDVASIPTDLYFAV 240

QY 241 GIHSPEVFRNLLHFARMEFFDRTRTSTYVNFRIISNLVLYLVIIHWNACIYYVSK 300
DB 241 GIHSPEVFRNLLHFARMEFFDRTRTSTYVNFRIISNLVLYLVIIHWNACIYYVSK 300

QY 301 SIGFGVDTWVYNTDPEYGLAREIYICLYWSTLTLTITIGETPPVKDEEYLVFVDFL 360
DB 301 SIGFGVDTWVYNTDPEYGLAREIYICLYWSTLTLTITIGETPPVKDEEYLVFVDFL 360

QY 361 IGVLI FATVGVSGMISNMNATRAEFOAKIDAVKHVQFRKVKDKMEAKVIKWFYDLWT 420
DB 361 IGVLI FATVGVSGMISNMNATRAEFOAKIDAVKHVQFRKVKDKMEAKVIKWFYDLWT 420

QY 421 NKKTVDREVLKNLPKAKRAEIAINVHLSTLKKVRIPODWBAGLLVELVLKLPQVSPG 480
DB 421 NKKTVDREVLKNLPKAKRAEIAINVHLSTLKKVRIPODWBAGLLVELVLKLPQVSPG 480

QY 481 DYICRKGDIGKEMYIIKEGKLVAVDDGVTOYALLSAGSCFGEISILNKGSKMGNRTA 540
DB 481 DYICRKGDIGKEMYIIKEGKLVAVDDGVTOYALLSAGSCFGEISILNKGSKMGNRTA 540

QY 541 NIRSIGYSLDFCLSKDDLMVEATEAPDAKKVLEERGRELKMGLLDENEVAASVEDVQ 600
DB 541 NIRSIGYSLDFCLSKDDLMVEATEAPDAKKVLEERGRELKMGLLDENEVAASVEDVQ 600

QY 601 EKLEQLETNMDLYTRFARLLAEYGAQOKLQRTITVLETKMKQNHEDDYLSDGINTPEP 660
DB 601 EKLEQLETNMDLYTRFARLLAEYGAQOKLQRTITVLETKMKQNHEDDYLSDGINTPEP 660

QY 661 TAEE 664
DB 661 AVAE 664

RESULT 2

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Q8CFV6 PRELIMINARY; PRT; 631 AA.
ID Q8CFV6
AC Q8CFV6;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein (Cng3 protein).
GN CNG3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC035272; AAH35272.1; -.
DR EMBL; BC049145; AAH49145.1; -.
DR PLR; MG1.1341818; Cng3.
DR MGD; MGI.1341818; Cng3.
DR GO; GO:0005221; F.intracellular cyclic nucleotide activated c. . . ; IPI.
DR InterPro; IPR000595; cNMP_binding.
DR InterPro; IPR005821; ion_trans.
DR InterPro; IPR001622; K+channel_pore.
DR Pfam; PF00027; cNMP_binding; 1.
DR Pfam; PF00520; ion_trans; 1.
DR SMART; SM00100; cNMP; 1.
DR PROSITE; PS00888; cNMP_BINDING_1; 1.
DR PROSITE; PS00889; cNMP_BINDING_2; 1.
DR PROSITE; PS00042; cNMP_BINDING_3; 1.
KW Hypothetical protein.
SQ SEQUENCE 631 AA; 72701 MW; 4FAD66E3A8A3FE6C CRC64;

Query Match          62.2%; Score 2160.5; DB 11; Length 631;
Best Local Similarity 67.0%; Pred. No. 1.3e-151;
Matches 412; Conservative 85; Mismatches 93; Indels 25; Gaps 5;

QY 57 EMDPRRGGGQFRIVLGVIRDWANKNFREPRDPSFLFRGPELQVTTTHQ---- 112
DB 24 DLDHVENGLG---RVSRLLIISIRAWASHLHDEQCTPDSFLDRFHGSELKEVSTRESNAQ 80

QY 113 ---GDDKGGKDGEGKGTGKKFELFVLDAGDWYRWLFVAMPVLYNWCLLVARACFSDL 169
DB 81 PNPGEQKPPDGGEG---RKEEPIVDPSSNIYYRWLTALPVPYFNWCLLVCRACFDEL 136

QY 170 QNRFVFWWLVLDDPSDVTYIADLIIRLTGFEQGLLVKDPKLRDNYHTLOFKLDVAS 229
DB 137 QSEHLTLVLVDYSADVLVLDIVRARTGFEQGLMWVRDTRKRLWKHYTKLHFKLDILS 196

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QY 451 LKVRIFQDWEAGLLVVLKLPQVSPGDYICRKGDIGKEMYYIKGKLVAVDDGVT 510
DB 817 LKRVFQNTAEGLCELVLRLPFLVSPGDYICRKEVGKEMYIVNRLQVAVDNGKT 876
QY 511 QYALLSAGSCFGEISILNKGSKMGNRTANIRSLGYSDFCLSKDLMBAVTEAPDAK 570
DB 877 VMASLKAGSYFGEISILNM--GTAGNRTASVRSVGSDFVLSKKDMWDVLKEYPAARV 934
QY 571 VLE 573
DB 935 RLE 937

RESULT 14
Q9QX26 PRELIMINARY; PRT; 252 AA.
AC Q9QX26;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cyclic nucleotide-gated cation channel (Fragment).
GN CNG3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Qiu W., Guggino S.E.;
RT "Cyclic nucleotide-gated cation channel (CNG3) expression in rat
kidney.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF031943; AAB87065.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005267; F:potassium channel activity; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR000595; cNMP binding.
DR Pfam; PF00027; cNMP binding; 1.
DR SMART; SM00100; cNMP; 1.
DR PROSITE; PS00888; cNMP BINDING_1; 1.
DR PROSITE; PS00889; cNMP BINDING_2; 1.
DR PROSITE; PS00042; cNMP BINDING_3; 1.
FT NON TER 1 1
FT NON TER 252 252
SQ SEQUENCE 252 AA; 28677 MW; C59A1CF7654AA894 CRC64;

Query Match 32.5%; Score 1128; DB 11; Length 252;
Best Local Similarity 85.3%; Pred. No. 1.4e-75;
Matches 214; Conservative 21; Mismatches 16; Indels 0; Gaps 0;

QY 317 PEYGLAREYICLYWSTLTITIGETPPPPVKDEYLFVDFLIGLIVFATIVGVNYSM 376
DB 2 PEYGLSRKVIYSLYWSTLTITIGETPPPPVKDEYLFVDFLIGLIVFATIVGVNYSM 61
QY 377 ISNNATRAEFQAKIDAVKHYMQPRKYSKMEAKVIKWFYLTWNTKKTVDREVLYKNLPA 436
DB 62 ISNNATRAEFQAKIDSIKQTMQPRKVTQDLETRVIRWFDYLVANRKTVDKEVLYKNL 121
QY 437 KLRAEIAINVHLSTLKKVRIFQDWEAGLLVVLKLPQVSPGDYICRKGDIGKEMYYIK 496
DB 122 KLRAEIAINVHLSTLKKVRIFQDWEAGLLVVLKLPQVSPGDYICRKGDIGKEMYYIK 181
QY 497 KEGKLVAVDDGVTQYALLSAGSCFGEISILNKGSKMGNRTANIRSLGYSDFCLSKD 556
DB 182 KEGKLVAVDDGVTQYVVLSDGSYFGEISILNKGSKMGNRTANIRSLGYSDFCLSKD 241
QY 557 DLMEAVTEAPD 567
DB 242 DLMETLTYPE 252

RESULT 15

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Q9USE2 PRELIMINARY; PRT; 1463 AA.
AC Q9USE2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CNG channel-like.
GN CNGL OR CG9176.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Miyazu M., Tanimura T.;
RT "A putative CNG-channel of Drosophila melanogaster.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB030577; BAA89278.1; -.
DR FlyBase; FBgn0029090; cngl.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005267; F:potassium channel activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR000595; cNMP binding.
DR InterPro; IPR005821; Ion Trans.
DR InterPro; IPR001622; K+channel_pore.
DR Pfam; PF00027; cNMP binding; 1.
DR Pfam; PF00520; ion Trans; 1.
DR SMART; SM00100; cNMP; 1.
DR PROSITE; PS00888; cNMP BINDING_1; 1.
DR PROSITE; PS00889; cNMP BINDING_2; 1.
DR PROSITE; PS00042; cNMP BINDING_3; 1.
KW Ionic channel; Transmembrane.
SQ SEQUENCE 1463 AA; 159935 MW; D902602E351D42C2 CRC64;

Query Match 30.7%; Score 1068; DB 5; Length 1463;
Best Local Similarity 35.6%; Pred. No. 5.2e-70;
Matches 234; Conservative 136; Mismatches 206; Indels 82; Gaps 15;

QY 80 DWANKNFR-----EEEP---RPDSFLERF---RQPELQTVTTHQDDKGGK 119
DB 39 DWTRSNQRWMLRTTVQISSAIQKPKLREDSFLKRFSTRQIPETQETVEDTGSASG 98
QY 120 DGEKGKTKKKFELF-----VLDPAQWYRVLVFIAMPVLYNWLCLVARCFSDLQNYF 174
DB 99 DVD-KSVKRRRVLQKRSSVNDENEFYFWLMLVCLVLYNLTILVROSPFELQSV 157
QY 175 VVWLVDYFSDTVYIADLIIRLTGFLQGLLVKDPKKRDNYHTLQFKLDVASIIPD 234
DB 158 TFWLICDSMTDVVFIIDIIIVQLATGYLEQGLMYDDRLKACHYVHSRDETFDMLIPLD 217
QY 235 LIYPAGVGHSPREVRNLLHFARMEFEEDRTSTYPNIFRISNLVLYLVIHWNACI 294
DB 218 LLQLKMGTH-PLURFTRFFKVSRYFYIVESTVWPNLRVNLHILLILAHFGCF 276
QY 295 YVVISKISIGFVDTWYYPNITDEPYGLARBYTYCLYWSLTTLTIGETPPPVKDEEYLF 354
DB 277 YFLSEAGFGQD-WVYP-YRPGDYPLTRKYLGLSYWSTLTTLTIGDLTPETNAEYIF 334
QY 355 VIFDFLIGLIVFATIVGVNYSMISNNATRAEFQAKIDAVKHYMQPRKYSKMEAKVIK 414
DB 335 TIVSYLIGVIFATIVGVNVTNRNARLEFERLLDGAKTYMRHHKVPFGMKRRVLR 394
QY 415 FDYLTWNTKTV---DEREVLKNLPAKLRAEIAINVHLSTLKKVRIFQDWEAGLLV 471
DB 395 YDYSWNRGRITQGGGDINTALGLLPDKLTALHVNLSVLKVTIIFQEQPFELHDLVLK 454
QY 472 LRQVSPGDYICRKGDIGKEMYYIKGKLVAVDDGVTQYALLSAGSCFGEISILNKG 531
DB 455 MKAYITFGDSICRKEGVAEREMFIADGILEVLSETGKV-LTTMKAGDFGEIGILNLDG 513

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QY 532 SKMGNRTANIRSLGYSDLFCLSKDDLMEAVTEAPDAKKVLBERGREILLMMGLLDENEV 591
Db 514 L---NKRTADVRSVGYSELSFSLREDVLAAMKDYFDAQEIIQTLGRKELMEVRCVNKKYA 570
QY 592 AASMEVDV-----QEKLEQLETNMDTLYTREA-RLLAEYTGAAQOKLKQRI 635
Db 571 KAQSDKEAAAYAAAHPHHHQSHHQVHQSDSENSASAKIIVDKLKHVDVGFRNVLKKSR 630
QY 636 T-----VLETKMKQNHEDDYLSDGI-----NPIEPTAA 663
Db 631 TSRKSDSELEMOPLHNTSPRGSKILLKRMRSVRDEKDDSAEAKDELHDKTSPFIGA 688

Search completed: May 12, 2004, 11:15:12
Job time : 47 secs